STIC-Biotech/ChemLib

Fr m: Sent: T:

Subject:

Li, Ruixiang Wednesday, March 19, 2003 10:56 AM STIC-Biotech/ChemLib Sequence search of Application NO: 09/727,739

Please do a standard search on:

(i) SEQ ID NOS: 15 and 18 against the interference amino acid databases;

(ii) SEQ ID NOS: 17 and 19 against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li GAU 1646 CM1 10E18 Mail Box 10D19 306-0282

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Point of Contact	
P. Sheppard	
Telephone number: (703) 308-44	199

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed: 3/2 5/03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.) STN: DIALOG: Questel/Orbit: DRLink:_

Lexis/Nexis: Sequence Sys.: WWW/Internet: Other (specify): Sequence 132, App Sequence 380, App Sequence 380, App Sequence 380, App Sequence 132, App Sequence 132, App Sequence 132, App Sequence 132, App Sequence 380, App Sequence 380, App Sequence 5, App11 Sequence 5, App11 Sequence 7, App11 Sequence 7, App11 Sequence 11, App11 Sequence 12, App11 Sequence 137, App11 Sequence 11, App11

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US-10-142-423-380
US-09-766-396-5
US-10-062-375-5
US-10-101-487-52
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-09-766-396-10
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                                                                                                                            March 21, 2003, 11:53:33 ; Search time 21.4378 Seconds (without alignments) 276.816 Million cell updates/sec
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1 MRVSQIHCALALLGLALAIC......PPRERKAGCKNFYWKGFTSC 111
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/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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trodata/1/pubpaa/PCT_NEW_PUB.pep:*
trodata/1/pubpaa/US06_NEW_PUB.pep:
trodata/1/pubpaa/US06_PUBCOMB.pep:
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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./pubpaa/US09_PUBCOMB
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                                                                                                                                                                                                                                                                                                                                                                                    221153 seqs, 53462247 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*
                                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Summaries

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160.5 26.9 110 10 18-09-766-396-3 Sequence 3, Appliant of the control o

Result No. Sequence 132, 7 Sequence 380, 4 Sequence 132, 4 Asquence 132,

80.08

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TTLE OF INVENTION: DNAS ENCODING NEW FUSION PROTEINS AND PROCESSES FOR TILLE OF INVENTION: PREPARING USEFUL POLYPEPTIDES THROUGH EXPRESSION OF THE TILE OF INVENTION: DNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT: TOMPKINS, CHRISTOPHER K.
PPLICANT: WAGGONER JR., DAVID W.
ITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
                                                                                                   51 LSEPNOTENDALEPEDLPQAAEQDEMRLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 - CPLSHDGYCLHDGVCMYIEALDKYACNCVVGYIGERCQYRDLKWWELRDYDIPTTENLY 110
                      2 CALAALCIVLALGGVTGAPSDPRL----RQFLQKSLAAA----TGKQELAKYFLAE---L 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SQIHCALALIGLALAICSQGAA--SQPDLDLASRRILQRALAAALPHRSGVSERWRTFYP 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Designated OTHER INFORMATION: an amino acid sequence of OTHER INFORMATION: MWPSp-MWPmp20-(His)6-EGF-TEV-Somatostatin 28 US-09-280-030-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.7%; Score 105.5; DB 10; Length 140; 28.0%; Pred. No. 0.00015; Live 18; Mismatches 35; Indels 55;
                                                              67 RWRPRKVKGPQLKAKE------DLERSVDNLP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: JP10-87339/1998
EARLIER FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/280,030A CURRENT FILING DATE: 1999-03-26
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BERGMAN, PHILIP A.
LOFQUIST, ALAN
PIETZ, GREGORY E.
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Best Local Similarity 28.0%
Matches 42; Conservative
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SOFTWARE: PS
SEQ ID NO 64
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                                                                                                                                                                                                                                                      2 CALAALCIVLALGGVTGAPSDPRL----RQFLQKSLAAA----TGRQELARYFLAE---L 50
                                                                                                                                                                                        30; Indels '27; Gaps
                                                                                                                                                                                                                           8 CALALLGLALAICS-QGAASQPDLDLASRRLLQRALAAALPHRSGVSERWRTFYPNCPCL 66
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STREET: 10666 No. US20020133000Alth Torrey Pines Road, TPC-6
                                                                                                                                                Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9e-11;
ss 30; Indels 27;
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                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Siggins, Steven J. Henrikse, Steven J. Henrikse, TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                           26.9%; Score 160.5; DB 38.3%; Pred. No. 7.9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/062,375-
FILING DATE: 30-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches
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TOPOLGGY: linear

MOLECULE TYPE: protein
FRAGMENY TYPE: C-terminal
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-766-396-3
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FRAGMENT TYPE: C-terminal
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-062-375-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sutcliffe, Gregor J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10062375 Patent No. US20020133000A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     de Lecea, Luis
Siggins, George R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
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                                                                                                                                                                  Local Similarity 38.39 ces 46; Conservative
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46; Conserv
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38; Gaps
                                         62 -----EWASQDSSSTAFEGGTPELSKRQ--ERPPLQQPPHRDKKPCKNFFWKTFSSC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 YPNCPCLRWRPRKVKG-----PQLKAKEDLERSVDNLPPRERKAGCKNFYWKGFTSC 111
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ilarity 25.5% pred No. 0.014;
Conservative 9; Mismatches 42; Indels
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10666 No. US20020133000Alth Torrey Pines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICATION NUMBER: US/10/062,375 ILING DATE: 30-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sutcliffe, Gregor J
                                                                                                                                                                                                                                                                     Henriksen, Steven TITLE OF INVENTION: CORTISTAT
                                                                                                                                                 Application US/10062375
US20020133000A1
                                                                                                                                                                                                                  Surcial de Lecea, Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                            California
                                                                                                                                                                                                           APPLICANT: Sutcliffe,
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
  60 YPNCPCLRWRPRKVKG---
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Matches 30; Conserve
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                                                                                                ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic fusion of -0.11ER INFORMATION: protein US.10-101-487-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: THE SCRIPPS RESEARCH INSTITUTE
10666 No. US20020013456Alth Torrey Pines Road, TPC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.6%; Score 87; DB 10; Length 112; 25.2%; Pred. No. 0.014;
                                                                                                                                                                                     Score 88; DB 9; Length 200;
Pred. No. 0.021;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Indels
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NG DATE: 18-Jan-2001
                                                                                                                                                                                                                                                                     81 KEDLERSVDNLPPRERKAGCKNFYWKGFTSC 111
                                                                                                                                                                                                                                                                                             170 EEEEEEEEEEEEEEEEEGCKNFFWKTFTSC 200
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TION NUMBER: 08/857,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-766-396-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sutcliffe, Gregor J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LING DATE: 18-Jan
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ZENTION: CORTISTATI
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ER READABLE FORM:
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Siggins, George R
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09766396
Patent No. US20020013456A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION DATA:
                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                Ouery Match
Best Local Similarity 48.4%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESS
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Best Local Similarity
Matches 30; Conserv
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SEQ ID NO 53
LENGTH: 200
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US-09-766-396-2
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10666 No. US20020013456Alth Torrey Pines Road, TPC-8
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 83; DB 12;
Pred. No. 0.029;
5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-10-062-375-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPA
OPERATING SYSTEM: PC-DO
                                                                                                                                                                                                                                                                                                                                                                                                                      13.9%;
llarity 44.4%;
Conservative
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                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION
                                                                   PRIOR APPLICATION
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Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                               SEQUENCE
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STREET: 10666 No. US20020133000Alth Torrey Pines Road, TPC-6
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Best Local Similarity 44.4%; Pred. No. 0.029;
Matches 16; Conservative 5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 PQLKAKEDLERSVDNLPPRERKAGCKNFYWKGFTSC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ION NUMBER: US/09/766,396
ATE: 18-Jan-2001
CATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                             NUMBER: 08/857,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE: C-terminal SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-09-766-396-6
Henriksen, Steven J
TITLE OF INVENTION: CORTISTATI
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                                                                                                                                                                                                                                                                                APPLICATION DATA:
                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                      STATE: California
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                                                                                                                     La Jolla
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INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC RIVENTION: ACIDS ENCODING THE SAME
                                                                                        37; Indels 19; Gaps
                                                                                                                                  ----WRPRKVKGPQL-KAK 81
                                                                                                                                                                           11 LLSGATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEA 70
                                                   Length 105;
                                                                                                                                                                                                                     82 EDLERSVDNLPP----RERKAGCKNFYWKGFTSC 111
                                            Ouery Match 13.5%; Score 80.5; D Best Local Similarity 27.7%; Pred. No. 0.07 Matches 26; Conservative '12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATION NUMBER: US/10/066,500
                                                                                                                                  37 LLQRALA-AALPHRSGVSERWRTFYPNCPCLR
    JS-10-062-375-26
                                                                                                                                                                                                                                                                                                                                                     37; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                37 LLQRALA-AALPHRSGVSERWRTFYPNCPCLR-------WRPRKVKGPQL-KAK 81
                                                                                                                                                                                                                                  13.5%; Score 80.5; DB 10; 27.7%; Pred. No. 0.07; ive 12; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                 71 REVARROEGAPPQQSARRDRMPCRNFFWKTFSSC 104
                                                                                                                                                                                                                                                                                                                                                                                                      82 EDLERSVDNLPP----RERKAGCKNFYWKGFTSC 111
                                                                                                                                  FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-766-396-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/062,375
FILING DATE: 30-Jan-2002
CLASSIFICATION: <UNKNOWN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/10062375
Patent No. US/202013133000A1
GENERAL INFORMATION:
GRIERAL INFORMATION:
APPLICANT: Sutcliffe, Gregor J.
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MEDIUM TYPE: Floppy disk
LENGTH: 105 amino acids TYPE: amino acid:
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Best Local Similarity 27.77
Matches 26; Conservative
                           TYPE: amino aci
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NUMBER: PCT/US98/14552 1998-07-14 NUMBER: PCT/US98/18824 1998-09-10 MBER: PCT/US98/19093 998-09-14 NUMBER: PCT/US98/19330 1998-09-16 PCT/US98/24855 PCT/US98/25190 PCT/US99/05028 PCT/US98/19437 PCT/US98/25108 PCT/US99/12252 PCT/US99/20111 PCT/US99/20594 PRIOR APPLICATION NUMBER: PCT/US99/21547 e: 2001-06-01 N NUMBER: 09/886342 : 2001-06-19 NUMBER: 09/886342 NUMBER: 09/380138 1999-08-25 MBER: 09/808689 001-03-14 MBER: 09/664610 000-09-18 7767609 /802706 MBER: 09/870574 7380137 /380139 403296 403297 /522342 /548815 /665350 /709238 7866028 /423741 /423844 MBER: 09/8 001-03-09 MBER: 09/ MBER: 09/ MBER: 09/ MBER: 09,

13.5%; Score 80.5; DB 9; Length 155;

Query Match

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7063738
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                                                       61 LLSGATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEA 120
                                37 LLQRALA-AALPHRSGVSERWRTFYPNCPCLR-------WRPRKVKGPQL-KAK 81
              19;
           37; Indels
Best Local Similarity 27.7%; Pred. No. 0.11;
Matches 26; Conservative 12; Mismatches
                                                                             82 EDLERSVDNLPP----RERKAGCKNFYWKGFTSC 111
                                                                                             Sequence 380, Application US/10028072
Publication No. US20030004311A1
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PRIOR FILING DATE: 1997-
PRIOR APPLICATION NUMBER
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US-10-028-072-380
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFREENCE: P3330R1C17
CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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                                                           61 LLSGATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEA 120
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    ---WRPRKVKGPQL-KAK 81
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13.5%; Score 80.5; DB 9; Length 155;
Best Local Similarity 27.7%; pred, No. 0.1;
Matches 26; Conservative 12; Mismatches 37; Indels 19
Matches 26; Conservative 12; Mismatches 15; Conservative 15; Mismatches 15; Conservative 15; Mismatches 15; Conservative 15; Mismatches 15; Conservative 15; Conserva
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                                                                                                                                           82 EDLERSVDNLPP----RERKAGCKNFYWKGFTSC 111
                                                                                                                                                                                                  121 REVARROEGAPPOQSARRDRMPCRNFFWKTFSSC 154
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37 LLORALA-AALPHRSGVSERWRTFYPNCPCLR
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US-10-121-049-380
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PRIOR APPLICATION NUMBER: 60/086430
PRIOR FILING DATE: 1998-05-22
PRIOR PELING DATE: 1998-05-28
PRIOR PLILING DATE: 1998-05-28
PRIOR PLILING DATE: 1998-05-28
PRIOR PLILING DATE: 1998-06-04
PRIOR PLILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088730
PRIOR APPLICATION NUMBER: 60/088741
PRIOR APPLICATION NUMBER: 60/088741
PRIOR APPLICATION NUMBER: 60/08878
PRIOR PLILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-10
PRIOR PLILING DATE: 1998-06-11
PRIOR PLILING DATE: 1998-06-11
PRIOR PLILING DATE: 1998-06-11
PRIOR PLILING DATE: 1998-06-12
PRIOR PLILING DATE: 1998-06-13
PRIOR PLILING DATE: 1998-06-13
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PRIOR PLILING DATE: 1998-06-26
PRIOR PLILING DATE: 1998-07-01
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PRIOR PLILING DATE: 1998-07-07
PRIOR PLILING DATE: 1998-07-07
PRIOR PLILING DATE: 1998-07-07
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998-05-07
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Best Local Si
Matches 26;
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61 LLSGATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEA 120
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0.11;
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Pred. No. 0.11;
12; Mismatches 37; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :: | .: || | : |:|| || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 111 || 
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Best Local Similarity 27.77
Matches 26; Conservative
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Best Local Similarity 27.7
Matches 26; Conservative
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S-10-123-904-380
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ORGANISM: Homo Sapien
US-10-140-470-380
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Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl1
Sequence 1, Appl1
Sequence 1, Appl1
Patent No. 5212156
Patent No. 5268278
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                                                                                                                                                                     Sequence
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SUCCLIFFE, Gregor J.
APPLICANT: Ge Lecca, Luis
TITLE OF INVENTION: CORPISTATIN: NEUROPEPTIDES,
TITLE OF INVENTION: CORPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10666 No. 6074872th Torrey Pines Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                  100-414B-88
                                                                            US-09-331-405-1
US-09-196-259-1
US-09-196-259-1
5268278-4
US-09-100-414B-8
US-09-100-414B-8
US-09-100-414B-8
                                                                 1-991B-1
                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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APPLICATION NUMBER: US/08/648,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08648322
Patent No. 6074872
GENERAL INFORMATION:
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3R: 519
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REGISTRATION NUMBER: 34,16
REFERENCE/POCKET NUMBER: 5
LECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 110 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
FRAGMENT TYPE: C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.99
Best Local Similarity 38.33
Matches 46; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS.
LENGTH: 110 amino acid.
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COMPUTER READABLE FORM:
MEDIUM TYPE: FlOPPY C
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CITY: La JOLIA
STATE: California
COUNTRY: US
ZIP: 92037
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DD.
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155.808 Million cell updates/sec
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                                                                                                                                                                             US-09-727-739B-15
597
1 MRVSQIHCALALLGLALAIC......PPRERKAGCKNFYWKGFTSC 111
                                                                                                            March 21, 2003, 11:41:02; Search time 20.9614 Seconds
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... /cgn2_6/ptodata/2/laa/5A_COMB.pep:*

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... /cgn2_6/ptodata/2/laa/6A_COMB.pep:*

... /cgn2_6/ptodata/2/laa/PGTUS.COMB.pep:*

... /cgn2_6/ptodata/2/laa/PCTUS.COMB.pep:*

... /cgn2_6/ptodata/2/laa/PCTUS.COMB.pep:*

... /cgn2_6/ptodata/2/laa/PCTUS.COMB.pep:*
           GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                 262574 segs, 29422922 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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RESULT
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      --- PRERKAGCKNFYWKGFTSC 111
                      51 LSEPNQTENDALEPEDLPQAAEQDEMRLELQRSANSNPAMAPRERKAGCKNFFWKTFTSC 110
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                                                                                                                                                                                                                                                                                                     10666 No. 6074872th Torrey Pines Road, TPC-8
                                                                                                                                                                                               ) Lecea, Luis
WILON: CORTISTATIN: NEUROPEPTIDES,
WILON: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : OLSEN, HENRIK S.
: RUBEN, STEVEN M.
INVENTION: CORTISTATIN POLYPEPTIDES
                                                                                                                                                                                                                                                                                     THE SCRIPPS RESEARCH INSTITUTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 CSOGAASOPDLDLASRRLLORALAAALPHRSGVSER---
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Pred. No. 0.0(
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/648,322
                                                                                                                                                                               Sutcliffe, Gregor J. .
                                                                                                                Sequence 2, Application US/08648322
Patent No. 6074879
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6232100
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illarity 25.2%;
Conservative 9
67 RWRPRKVKGPQLKAKE----
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SEQUENCE CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DA APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                      La Jolla
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 -----EWASQDSSSTAFEGGTPELSKRQ--ERPPLQQPPHRDKKPCKNFFWKTFSSC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Indels
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Succiffe, Gregor J.
de Lecea, Luis
VENTION: CORTISTATIN: NEUROPEPTIDES
VENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 87; DB 4;
Pred. No. 0.0018;
9; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 CSQGAASQPDLDLASRRLLQRALAAALPHRSGVSER---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : THE SCRIPPS RESEARCH INSTITUTE 10666 No. 6074872th Torrey Pines
                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,980
FILING DATE: 31-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                     UMBER: US 60/037,386
07-FEB-1997
                                         APPLICATION NUMBER: US/09/001,472
FILING DATE: Herewith
Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/08648322
Patent No. 6074872
                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
LECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 14.6%;
Best Local Similarity 25.2%;
Matches 30; Conservative
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                 CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-09-001-472-3
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APPLICATION NUMBER:
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                                                                                                                                                                                        APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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OPERATING SYSTEM
                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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us-09-727-739b-15.rai

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11 LLSGATATAALPLEGGPTGRDSEHMQEAAGIRKSSLLTFLAWWFEWTSQASAGPLIGEEA 70
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    --WRPRKVKGPQL-KAK 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 79.5; DB 3; Length 109;
Pred. No. 0.016;
4; Mismatches 35; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                     : THE SCRIPPS RESEARCH INSTITUTE
10666 No. 6074872th Torrey Pines Road, TPC-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/648,322
FILING DATE:
                                                                                                                                                                                                                                                                    APPLICANT: Sutcliffe, Gregor J.
APPLICANT: de Lecea, Luis
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 POLKAKEDLERSVDNLPPRERKAGCKNFYWKGFTSC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 GTPGLSKSQERPPPQQPPHLDKKPCKNFFWKTFSSC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOSITIONS AND METHODS
                                                                                                    71 REVARROEGAPPQOSARRDRMPCRNFFWKTFSSC 104
    37 LLORALA-AALPHRSGVSERWRTFYPNCPCLR
                                                                                                                                                                                                           Sequence 5, Application US/08648322
Patent No. 6074872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08648322
Patent No. 6074872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          utcliffe, Gregor J.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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LECOMMUNICATION INFORMATION
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Best Local Similarity 31.2%;
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: La Jolla
STATE: California
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US-08-648-322-5
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                                                                                                                                                                                                                                                                      Length 85;
                                                                                                                                                                                                                                                                                                           13; Indels
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                                                                                                                                                                                                                                                                      Score 83; DB 3;
Pred. No. 0.0041;
5; Mismatches 1
                                                                                                                                                                                                                                                                                                                                              76 POLKAKEDLERSVDNLPPRERKAGCKNFYWKGFTSC 111
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                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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APPLICATION NUMBER: US 60/033,980
FILING DATE: 31-DEC-1996
PRIOR APPLICATION DATA:
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07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/09001472
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                                                                                                                                                                                                                                                                 13.9%;
llarity 44.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-FEB-1997 ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
REGISTRATION NUMBER: 34.
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMAT.
                                                                                                                                                                                       MOLECULE TYPE: protein
FRAGMENT TYPE: C-terminal
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Best Local Similarity 27.7
Matches 26; Conservative
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NUMBER OF SEQUENCES:
                                                          (619)
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Best Local Similarity
Matches 16; Conserv
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                                                                                           INFORMATION FOR
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                                                                              TELEFAX:
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2; Mismatches
                                                                                                13.1%; Score 78; 51.9%; Pred. No.
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                                                                                                                                                                        85 ERSVDNLPPRERKAGCKNEYWKGFTSC 111
                                                                                                                                                                                                        2 ERPPPOOPPHLDKKPCKNFFWKTFSSC 28
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ilarity 51.9%;
Conservative
                                                                                                                    Best Local Similarity 51.9
Matches 14; Conservative
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MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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Best Local Similarity
Matches 14; Conserv
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FRAGMENT TYPE:
                                                                   US-08-648-322-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Length 29;
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COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 13.1%; Score 78; DB Local Similarity 51.9%; Pred. No. 0.00 nes 14; Conservative 2; Mismatches
                                                                                                                    Patentin Release #1.0, Versi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/648,322
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                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/648,322
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                                                                                                                                                                                                             INFORMATION:
                                           COMPUTER READABLE FORM:
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STATE: California
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ITLE OF INVENTION:
                                                                                                                         SOFTWARE:
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Best Local S
Matches 14
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TTLE OF INVENTION: Production of Therapeutic Peptides in TTLE OF INVENTION: Transgenic Animals as a Fusion with Hemoglobin
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PatentIn Release #1.0, Version #1.25
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Sharma, Ajay
Khoury-Christianson, Anastasia
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5 Avenue of the Americas
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IBM PC compatible
                                                                                                            .7-NOV-1992
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Best Local Similarity 85.7
Matches 12; Conservative
                               CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTIC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1:
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OPERATING SYSTEM:
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                                                                                                                                                     CLASSIFICATION:
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SOFTWARE: PatentIn Release #1.0, Versión #1.25
CURROTT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                    : REED & ROBINS
285 HAMILTON AVENUE, SUITE 200
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31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible ODERATING SYSTEM: PC-DOS/MS-COGNICATION OF COMPUTED SYSTEM: PC-DOS/MS-COGNICATION OF COGNICATION OF COGNIC
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Eish & Richardso
225 Franklin Street
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llarity 85.7%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGCKNFFWKTFTSC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110-2804
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                           Chicago
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (312)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-286-748B-13
                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-08-676-263-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
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8
                                                                                                                                            Length 14;
                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                  Vincent, Jean-Pierre
daudriault, Georges
Beaudet, Alain
Beaudet, Alain
ENTION: FLUORESCENT SOMATOSTATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/416,007 FILING DATE: 04-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Fish & Richardson P.C. 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-676-263-11
Sequence 11, Application US/08676263
                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08416007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30,162
                                                                                                                                        Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
              ; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-255-272-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
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Best Local Similarity 85.7
Matches 12; Conservative
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                                                                                                                                                                                                       98 AGCKNFYWKGFTSC 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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COUNTRY: ULL
02110-7
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
Marshall, O'Toole, Gerstein, Murray & Borun
233 South Wacker Drive/6300 Sears Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 14;
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                               COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION DATA:
LOR APPLICATION NUMBER: EP 94300224.6
APPLICATION LUMBER: 12-JNH-1994
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
PPPLICATION NUMBER: US/08/676,263
FILING DATE: 07-NOV-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3, Application US/08286748B
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MEDIUM TYPE: 3.5" Disketie, 1.44 Mb
COMPUTER: IBM PS/2 Model SOZ or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/286,748B
FILING DATE: Advant 5, 1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/286,748B
FILING DATE: MWHER: 32,983
APPLICATION NUMBER: 32,983
APPLICATION NUMBER: 32,983
REPERENCE,DOCKET NUMBER: 32,983
REFERENCE,DOCKET NUMBER: 04547/013001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-6070
TELEPHONE: ADDITION: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: Inhear
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Search completed: March 21, 2003, 11:42:29. Job time: 21.9614 secs

Ouery Match 12.9%; Best Local Similarity 85.7%; Matches 12; Conservative

Oy Db

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095bx3 zea mays (m
09fer7 zea mays (m
007834 pseudomonas
09m6d8 oryza sativ
09p4a6 letharia vu
08zph5 salmonella
                             088768 oryza sativ
098798 oryza sativ
091799 neisseria m
09176 homo sapien
075175 homo sapien
075175 homo sapien
09172 oryza sativ
054501 streptomyce
090183 homo sapien
094843 streptomyce
               4 streptomyce
8 oryza sativ
1 rhizoblum 1
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Kakaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Actinopteryqii: Neopteryqii: Teleostei; Ostariophysi; Cypriniformes; Catostomidae; Catostomidae; Catostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRVSQIHCALALLGLALAICSQGAASQ--PDLDLASRRLLQRALAAALPHRSGVSERWRT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.2%; Score 136; DB 13; Length 120; Ilarity 34.6%; Pred, No. 71e-08; Conservative 16; Mismatches 18; Indels 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF292654; AAK97071.1; -
InterPro; IPR004250; Somatostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. AMAIN D.M., Youson J.H.; Al-Mahrouki A.A., Irwin D.M., Youson J.H.; Molecular cloning and characterization of white sucker preprosomatostatin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfan, PP03002; Somatostatin, 1.
SEQUENCE 120 AA; 13783 MW; 00828D35263E8805 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEWBLrel. 19, Created)
01-DEC-2001 (TrEWBLrel. 19, Last sequence update)
01-MAR-2002 (TrEWBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----WTKKDIEELLSQLSLPEIEAREN 75
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es 32; Conserv
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Matches
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                                                                                           March 21, 2003, 11:38:15; Search time 42.0773 Seconds (without alignments) 421.131 Million cell updates/sec
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                                                                                                                                                                                 450
1 MRVSQIHCALALLGLALAIC.....RWRPRKVKGPQLKAKEDLER 86
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098hg9
093w36
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082xp5
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090y40
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                   671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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score greater than or equal to
and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_bacteriap:*
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Maximum DB seq length: 200000000
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                                                                                                                                                                US-09-727-739B-17
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Perfect score:
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80.5
78.5
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                                                              OM protein
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                                                                                                 Run on:
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01-DEC-2001 01-DEC-2001 01-MAR-2002

ID DATE OF THE REPORT OF THE PROPERTY OF THE P

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Acipenser transmontanus (White sturgeon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Chondrostel; Acipenseriformes; Acipenseridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tostivint H., Lihrmann I., Sollars C., Vallarino M.,
                                                                                       Chordata, Craniata, Vertebrata, Euteleostomi, pterygii, Teleostei, Osteoglossomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chitala chitala (clown knifefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Polygenic expression of somatostatin in the sturgeon Acipenser transmontenus: molecular cloning and distribution of the mRNAs encoding two somatostatin precursors.";
J. Comp. Neurol. 00:0(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 93.5; DB 13; Length 114;
Pred. No. 0.0045;
4; Mismatches 12; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 88.5; DB 13; Length 116;
Pred. No. 0.017;
5; Mismatches 11; Indels 5;
                                                                                                                                                                                                                                                                                                         Al-Mahrouki A.A., Irwin D.M., Youson J.H.; Characterization of variant somatostatin cDNAs from several osteoglossomorphs: molecular identification and comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: AF291552: AAR97069 1; Interpretable of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02; Somatostatin; 1.
116 AA: 12616 MW; 72E0G3FF6C80650F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRVSQIHCALALLGLALAICSQGAA-SQPDLDLASRRLLQRALAAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MRVSQIHCALALLGLALAICSQGAASQPDLDLASRRLLQRALAA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLSSRIQCALALLSLALAVSSVSAAPS --- DLKLRQLLQRSLLA 41
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01-DEC-2001 (TrEWBLrel. 19, Last sequence update)
01-MAR-2002 (TrEWBLrel. 20, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                          Actinopterygii; Neopterygii; Teleostei, Ost
Osteoglossiformes; Mormyridae; Gnathonemus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
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InterPro; IPR004250; Somatostatin.
Pfam; PF03002; Somatostatin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.7%;
ilarity 54.3%;
Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 56.8%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M., LO.
Vaudry
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preprosomatostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I_TaxID=7904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Somatostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q90XE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q90Y40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
Q90XE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
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                                                                                                                                                                                                                  Osteoglossum bicirrhosum (sllver arawana).
Bukaryota: Medrazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Osteoglossidae; Osteoglossum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostel; Osteoglossomorpha;
Osteoglossiformes; Pantodontidae; Pantodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Al-Mahrouki A.A., Irwin D.M., Youson J.H.; "Characterization of variant somatostatin cDNAs from several osteoglossomorphs: molecular identification and comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of variant somatostatin cDNAs from several osteoglossomorphs: molecular identification and comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Score 108; DB.13; Length 114;
Pred. No. 0.0001;
9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ... LOUNAS from se comparated (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AFF292650, AAK9707.1; -1 InterPro; IPPR004250; Somatostatin. Pfam; PF03002; Somatostatin. SEQUENCE 115 h.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF295651; AAK97068 1;
Interpro; IPRO04250; Somatostatin.
Pfam; PF03002; Somatostatin; 1.
SEQUENCE 114 AA; 12352 MW; 7E3D44CB6A27B12F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRVSQIHCALALLGLALAICSQGAASQPDLDLASRRLLQRALAAAL, 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRVSQIHCALALIGLALAICSQGAASQPDLDLASRRLLQRALAAAL 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   090Y41 PRELIMINARY; PRT; 114 AA. 090Y41; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 112; DB 13;
Pred. No. 3 6e-05;
4; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Al-Mahrouki A.A., Irwin D.M., Youson J.H.; Characterization of variant somatostation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last seq
(TrEMBLrel. 20, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Butterflyfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 24.0%;
1 Similarity 50.0%;
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 56.59
nes 26; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-109271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preprosomatostatin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-8276;
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01-DEC-2001

TREE BY OCCOOR

Matches

QQ

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Q90Y42 Q90Y42;

Query Match

Matches

οý QQ

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01-OCT-2001 (TIBMBLrel. 18, Created)
01-OCT-2010 (TIBMBLrel. 18, Last sequence update)
01-OCT-2010 (TIBMBLRel. 21, Last annotation update)
                                               01-JUN-2002 (TrEMBLrel. 21, L
Hypothetical protein ml12874.
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-2371;
                                                                                                                                                                                                           NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical
SEQUENCE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coutinho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ariah M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Ariah M., Gillault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Cholsen N., Claudel-Renard C., Cunnac S., Demange Baspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T., Sigular P., Thebault P., Whalen M., Wincker P., Levy M., Welssenbach J., Boucher C.A.; Genome sequence of the plant pathogen Ralstonia solanacearum."
                                                                                                                                                                                                                                                                                                                                                                                  Query Match

17.9%; Score 80.5; DB 13; Length 114;
Best Local Similarity 50.0%; Pred. No. 0.13;
Matches 22; Conservative 6; Mismatches 13; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 78.5; DB 16; Length 603;
Pred. No. 1.2;
3; Mismatches 15; Indels 17;
                                                                                                                                                        "Characterization of variant somatostatin cDNAs from several osteoglossomorphs: molecular identification and comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                            Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF792653; AAK97070.1; --
Interpro; IPR004250; Somatostatin.
Ptem: PF03002; Somatostatin; 1.
SEQUENCE 114 AA; 12561 MW; 4E3C32F58E34F971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lidyltransferase; Complete proteome 66305,MW; 5A3A29A1674E541C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRVSQIHCALALIGLALAICSQGAASQPDLDLASRRLLQRALAA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLSTRIQCALALLSLALPVSSVYAAPS---DLKLRQLLQRSIIA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable DNA primase protein (EC 2.7.7.-).
DNAG OR RSC2216 OR RS01383.
                                                                                                                             Al-Mahrouki A.A., Irwin D.M., Youson J.H.; "Characterization of variant somatostatin
Actinopterygii; Neopterygii; Teleostel; O
Osteoglossiformes; Notopteridae; Chitala.
NCBI_TaxID=112163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 38.6
2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603 AA;
                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salstonia
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Best Local S
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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098HG9;

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., Yamada M., Tabata S.;
genome structure of the nitrogen-fixing symbiotic bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer P. Colombo C., Costa F.E., Costa M.C.R., Costa.Neto C., L., Cristofani M., Dias Neto E., Docena C., El-Dorry H., P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A., Farrora S.C., Franco M.C., Frohme M., Furlan L.R.,
Rhizobium loti (Mesorhizobium loti).
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                 Alkawa A., Adwasiiina A., Aimida ..., hara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.9%; Score 76; DB 16; Length 251; 33.3%; Pred. No. 0.97; tive 15; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nterpro: IPR001173; Glycos_transf_2.

dan, PF00535; Glycos_transf_2; 1.

ypotherical protein; Complete protecme.

EQUENCE 251 AA; 27987 MW; 45709C6A71EDD2AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
Hypothetical protein Xf2472.
                                                                                                                                                                                                                                            MEDLINE-21082930; Pubbmed-11214968;
Kaneko T., Nakamura Y., Sato S., Asa
Watanabe A., Idesawa K., Ishikawa A.
Kishida Y., Kiyokawa C., Kohara M.,
Mochizuki Y., Nakayama S., Nakazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 -- CLRYRLKLAVRRRLSAPKIELQSVL 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20365717; PubMed-10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 33.39
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress). Sukaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudlochyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Persoco B.R., Persetta G.A.G., Perseta H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E., Jr., de Sa R.G., Santelli N.V., Sansaski H.E., de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., Vallada H.V., Santelli N.V., Sansaski H.E., Vallada H. Van Silva M.M., dr.Y., Truffi D.Y., Tsai S.M., Tsuhako M.H., Yar Latz M.F., Truffi D., Tsai S.M., Tsuhako M.H., Zatz M., Meidanis J., Setubal J.C.; The genome sequence of the plant pathogen Xylella fastidiosa.", Nature 406:151-159(200).
                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                       DB 16; Length 435;
                                                                                                                                                                                                                                                                                                                      18; Indels
                                                                                                                                                                                         EMBL; AE004055, AAP85270.1; --
InterPro; IPR002604; AT2_TR2.
Pfam; PF01685; AT2_TR2, 1.
Hypothetical protein; Complete proteome.
SEQUENCE 435 AA; 47299 WW; E9272E57460CB447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Arabidopsis ORF clones.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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44863 MW; 5BB5AC7DAC436846 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                     15.2%; Score 68.5; I 33.9%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                    6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
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cDNA clones.";
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R000209; Peptidase_S8.
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8; SUBTILASE_SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel, 19, (TrEMBLrel, 19, (TrEMBLrel, 20,
                                                                                                                                                                                                                                                                                                   Local Similarity ... tes 20; Conservative
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Q93W36
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Eukaryota; Viridiplantes; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantes; Streptophyta; Embryophyta; Engellophyta; Englishyta; endicotyledons; core endicots; Rosidae; eurosids II; Brassicales; Brassicacea; Arabidopsis; Core endicots; Rosidae; NCBL_TaxID-3702;
                                                                                                                                                   Gaps
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Makaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids.II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                  GLALAICSOGAASQPDLDLASRRLLQRALAA---ALPHRSGVSERWRTFYPNCPCLRWRP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLALAICSOGAASOPDLDLASRRLLQRALAA---ALPHRSGVSERWRTFYPNCPCLRWRP 70
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Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
Lan X., Kaul S., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 GVSVIAAYTGAVSPTNEQFDPRRLLFNAISGTSMSCPHISGIAGLLKTRYPS----WSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin X., Kaul S., Shea T.P., Fujii.C.Y., Shen M., VanAken S.E., Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito Barnstead A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C. Eraser C.M., Venter J.C., Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, ACO0718; AAM15440.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%; Score 68; DB 10; Length 578; ilarity 28.1%; Pred. No. 18; Conservative 13; Mismatches 25; Indels
                                                                     25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            578 AA; 60733 MW; AFCAA0F484635E1C CRC64;
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21, Last annotation update)
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on update)
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01-50N-2002 (TrEMBLrel. 21, Last sequence update;
01-50N-2002 (TrEMBLrel. 21, Last annotation updai)
Subtilisin-like serine protease AIR3 (Fragment).
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01-301-2020 (TrEMBLrel. 21, Last sequence update)
01-301-2002 (TrEMBLrel. 21, Last senotation update)
Subtilisin-like serine protease AIR3 (Fragment).
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                                          ed. No. 13;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                  15.1%; Scc
28.1%; Pre
tive. 13;
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Ouery Match
Best Local Similarity 28.18
Matches 18; Conservative
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es 18; Conserv
                                                                                                                                                                                                                                                                  233 AAIR 236
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SEQUENCE
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Q8S896;
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Matches
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Q8S896
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Q8S8B0
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SASCILLE, FAUTC 700720;
MEDLINE-21534948; PubMed=11677609;
MEDLINE-21534948; PubMed=11677609;
MEDLINE-21534948; PubMed=11677609;
MEDLINE-21534948; PubMed=11677609;
MEDLINE-21534948; PubMed=11677609;
MEDLINE-21534948; PubMed=11677609;
Manand M., Sanderson K., Tali J., Dante M., Du F., Hou S., Layman D.
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Waterston R., Wilson R.K.,
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GLALAICSQGAASQPDLDLASRRLLQRALAA---ALPHRSGVSERWRTFYPNCPCLRWRP 70
                                                                                                                                                                                                                                                                                                                                "A novel subtilisin-like protease gene from Arabidopsis thaliana is expressed at sites of lateral root emergence.";
DNA Res. 6:13-19(1999).
                                                                                                                                                                                                                                                       STRAIN-CV. COLUMBIA;
MEDLINE-99246056; PubMed-10231025;
Neuteboom L.W., Veth-Tello L.M., Clljdesdale O.R., Hooykaas P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.1%; Score 68; DB 10; Length 772; Best Local Similarity 28.1%; Pred. No. 24; Matches 18; Conservative 13; Mismatches 25; Indels
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Hypothetical protein; Complete proteome: 9502F66 CRC64;
SEQUENCE 197 A5; 22326 MW; 7CAO59444F962F66 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   772 AA; 82873 MW; 75DCCA0DED63F47E CRC64;
  01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
subtilisin-like protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative periplasmic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00082; Peptidase_S8; 2.
R00723; SUBTILISIN.
PS00138; SUBTILASE_SER; UNKNOWN_1.
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Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                                    Res. 6:13-19(19-9).
L; AF098632; AAD12260.1; -:
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Jam; PF02225; PA; 1.
Jam; PF00082; Peptic
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Best Local Similarity
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NCBI_TaxID=602;
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PROSITE; PS00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protease.
SEQUENCE
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Begematophyta; Magnollophyta; eudloctyledons; core eudlocts; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GLALAICSOGAASOPDLDLASRRILORALAA---ALPHRSGVSERWRTFYPNCPCLRWRP 70
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                                                                                                                                                                  Length 755;
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al B.J.;
                           the EMBL/GenBank/DDBJ databases
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                                                                                                                    2E9BE365795936DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                             15.1%; Score 68; DB 10;
ilarity 28.1%; Pred. No. 24;
Conservative 13; Mismatches 25;
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PS00138; SUBTILASE_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
UNOV-1998 (TrEMBLrel. 08, Last seq
01.JUN-2002 (TrEMBLrel. 21, Last ann
Subtilisin-like protease (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-10080694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            interpro; IPR003137; PA.
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                                                                                            755
80844 MW;
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MEDLINE-99178779; Pubmed-10080
Meuteboom L.W., Ng J.M.Y., Kuy
Hooykaas P.J.J., van der Zaal
Fraser C.M., Venter J.C.;
Submitted (FEB-2002) to the
EMBL; AC007293; AAM15483.1;
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                                                                                            755 7
755 AA;
                                                                                                                                                                                     Local Similarity
es 18; Conserv
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SEQUENCE
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                                                                                                                                                                     Query Match
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                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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DB 16; Length 197;

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9; Mismatches 38; Indels 13; Gaps

Matches 30; Conservative

Search completed: March 21, 2003, 11:40:43 Job time : 46.0773 secs

GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

March 21, 2003, 11:35:23; Search time 10.3348 Seconds (without alignments) 345.142 Million cell updates/sec Run on:

Tille: US-09-727-739B-17
Perfect score: 450
Sequence: 1 MRVSQIHCALALIGLALAIC.....RWRPRKVKGPQLKAKEDLER 86

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues "Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	ption	oncorhynchu	carassius a		gallus gall	ictal	рошо	rana	protopterus	ovis aries	lophius ame	bos taurus	rhizobium s	bos taurus	saccharomyc	mus musculu	rattus norv	canis famil	sus scrofa	synechocyst	pseudomonas	escherichia	trypanosoma	trypanosoma	mus musculu	escherichia	mycobacteri	sus scrofa	anthocidari	homo sapien	chlamydomon	homo sapien	pasteurella	homo sapien
	Description	091194	09ygh4	09ygh5	P33094	P01171	P01166	P87384	09w7f0	046688	P01170	P26917	P55635	P29473	013374	P01167	P97874	P49670	028969	P74733	Q9hva4	Q8xaz3	P26338	026721	099p47	P76146	010709	028983	P15217	043323			09c119	09h9d4
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SUMMARIES	<u>0</u>	SMS2_ONCMY	SMS2_CARAU	SMSA_CARAU	SMS_CHICK	SMS1_ICTPU	SMS_HUMAN	SMS1_RANRI	SMS1_PROAN	SMS_SHEEP	SMS2_LOPAM	SMS_BOVIN	Y4RB_RHISN	NOS3_BOVIN	PT22_SACBA	SMS_MOUSE	GAK_RAT	SMS_CANFA	NOS3_PIG	ARCC_SYNY3	YAJ2_PSEAE	YNEE_ECO57	CYAA_TRYEO.		CTA4_MOUSE	YNEE_ECOLI	YLOO_MYCTU	ZAN_PIG	EGIP_ANTCR	DHH_HUMAN	TBC2_CHLRE	CTA3_HUMAN		PRDH HUMAN
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d	Query Match	77.2	26.4	20.3	18.6	17.9	17.7	17.0	16.8	15.4	15.4	15.2	15.0	14.9	14.7	14.6	14.3	14.1	14.0	13.8	. 13.7	13.4	13.4	13.4	13.4	13.2	13.2	13.2	13.1	13.0	13.0	13.0	12.9	12.9
	Score	347.5	119	ä	۳.	80.5	. ი	Ġ	75.5	۵.		œ.	67.5	. 67	99	ď.		63.5	63	9	61.5	. 60.5	60.5	60.5	60.5	59.5	59.5	59.5	59	58.5	ω.	₩.	. 28	28
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DNAB_RHOMR	TRL2_HUMAN	POL2_BAMMU	E4L2_MOUSE	E2K3_CAEEL	UL50_HCMVA	ORC5_YEAST	MSH5_HUMAN	SPA1_HUMAN	SPCR_HUMAN	NIFQ_AZOVI	DLX4_HUMAN
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12	12	12	12	12.8	12	12	12	12	12	12	12
28,	28	57.5	57.5	57.5	57	57	57	57	57	56.5	56.5

ALIGNMENTS

	RESULT SMS2_O ID S	LT 1 ONCMY STANDARD; PRT; 115 AA.
	125	2001 (Rel. 40, Creat 2001 (Rel. 40, Last
٠.	DE DE	16-OCT-2001 (Rel. 40, Last annotation update) Somatostatin II precursor [Contains: [Tyr21,Gly24]somatostatin-28;
	DE	[Tyr7,Gly10]somatostatin-14].
	308	Ouconivicinas myniss (naimos trout) (arimo gariumeri). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	88	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
	X O	
	RP	SEQUENCE FROM N.A.
	ZZ 6	MEDLINE=95354921; PubMed=7628684;
	R F	acterization of a cDNA encoding for
	E. E.	preprosomatostatin containing [Tyr7, Gly10]-somatostatin-14 from the
	R.	101. 98:253-261(199
	ပ္ပ	
	ខ្លួ	-!- SUBCELLULAR LOCATION: Secreted. -!- SIMILARITY: RELONGS TO THE SOMATIOSTATIN FAMILY.
	ខ្ល	
	8	This SWISS-PROT entry is copyright. It is produced through a collaboration
	ນູເ	between the Swiss Institute of Biolnformatics and the EMBL Outstation - the European Bioinformatics Institute There are no restrictions on its
j,	ဗ	non-profit institutions as long as its content is in no
	ខ្លួ	modified and this statement is not removed. Usage by and for commercial
	ខ	requires a incense in email to license@
	ပ္ပ	
	DR	EMBL; U32471; AAC59695.1; -
	D'R D'R	InterPro; IPRU0425U; Somatostatin. Pfam: PF03002: Somatostatin: 1
*	KW	
	1.	SIGNAL I LO POTENTIAL, PROPED 19 87 POTENTIAL
	FT	E 88 115 [
	FT	102 115 [TYR7,GLY10]SOMATOSTATIN-14.
	SQ .	DISULRID 104 115 BY SIMILARITY. SEQUENCE 115 AA; 12963 MW; 520595025FCA6D91 CRC64;
	Oue	77.2%; Score 347.
	Bes	Pred. No. 2.2e-32; 2; Mismatches 7;
	Οy	ت
	QQ	

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LUAGITYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Cyptiniotes; Carassius.
Cyptinidae; Carassius.
VCBI_TAXID-1957;
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12574 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Pancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHICK
                                                                                                                                                                                                        TISSUE-Brain
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Best Local S
Matches 23
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SMS_CHICK
DAS CHICK
DAT 01-0C
DT 01-0C
DT 01-0C
DE SOMBLE
SOMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tostatin; 1.
basic residues; Hormone; Signal; Multigene family.
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin X.-W., Peter R.E., Cloning and characterization of CDNAs encoding preprosomatostatin-I and -II from goldfish brain.".
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostom1;
Actinopteryg11; Neopteryg11; Teleoste1; Ostarlophys1; Cyprin1formes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Somatostatin IA precursor (Contains: Somatostatin-26; Somatostatin-
                                                                                                                                                                             J9YGH4, U9F1-2.
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last Contains: [Tyr21,Gly24]somatostatin-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 119; DB 1; Length 120; Pred. No. 1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYR21, GLY24|SOMATOSTATIN-28.
TYR7, GLY10|SOMATOSTATIN-14.
Y SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> RW (IN REF. 2).
98957D68011A651A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRVSQIHCALALLGLALAICSQGAASQ--PDLDLASRRLLQRALA 43
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                                                                                                                                                 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     terpro; IPR004250; Somatostatin.
am; PF03002; Somatostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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13723 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U60262; AAD09626.1;
EMBL; AF025686; AAF15306:1
                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7957;
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Q9YGH5;
                                                                                                                                                                                                                                                                                                                                                                                                              Cyprinidae;
                                                                                                                                                 SMS2_CARAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cleavage on pair of basic residues; Hormone; Signal; Multigene family. SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Lin X.-W., Peter R.E.; Cloning and characterization of CDNAs encoding preprosomatostatin-I and -II from goldfish brain."; Submittef (NOW 1995) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1993 (Rel. 27, Created)
-0-CCT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nate K., Kobayashi T., Karahashi K., Kato S., Yamamoto H., Yonekura H., Okamoto H., Yonekura H., Okamoto H., Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SOMATOSTATN INHIBITS THE RELEASE OF SOMATOTROPIN.
-!- SUBCELLULAR LOCATION: Secreted
-!- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 20.3%; Score 91.5; DB 1; Length 114; Local Similarity 54.8%; Pred. No. 0.0016; hes 23; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOMATOSTATIN-26 (POTENTIAL).
SOMATOSTATIN-14.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
B5920015E2D272A4 CRC64;
                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRVSQIHCALALLGLALAICSQGAASQPDLDLASRRLLQRAL 42
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outstation

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                                                                              noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
              between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Travis G.H., Sutcliffe J.G.;
Pravis G.H., Sutcliffe J.G.;
Phenol emulaion-enhanced DNA-driven subtractive cDNA cloning:
1solation of low-abundance monkey cortex-specific mRNAs.";
Proc. Natl. Acad. Sci. U.S.A. 85:1696-1700(1988).
Proc. Natl. Acad. Sci. U.S.A. 85:1696-1700(1988).
PROC. NATION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
-!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
-!- PHARMACEUTICAL: Available under the name Sandostatin (Novartis);
this is a synthetic cyclic analog known as octroctide or SNS
201-995. Used for the treatment of a variety of disorders
including acromegaly and the symptomatic treatment of carcinoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Macaca Fascicularis (Crab eating macaque) (Cynomolgus monkey):
Eukaryota: Wetazoa; Chordata: Craniata, Vertebrata; Euteleostomi,
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.9%; Score 80.5; DB 1; Length 114; 46.7%; Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                   1 24 PROBABLE.

101 114 SOMATOSTATIN-14.

103 114 E. -> Q (IN REF. 2).

114 AA; 12419 MW; FEE0F2C76F74D99F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ::| |||||| :||:||. || | | | |: |||: |
| MPSTRIQCALALLAVALSVCSVSGAPS----DAKLRQFLQRSILA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRVSQIHCALALLGLALAICS-QGAASQPDLDLASRRLLQRALAA 44
                                                                                                                                                                                                                                                      InterPro: IPKUV**...
Pfam: PE03002; Somatostatin; 1.
Charana on pair of basic residues; Hormone; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shen L.-P., Pictet R.L., Rutter W.J.;
"Human somatostatin I: sequence of the cDNA.";
Proc. Natl. Acad. Sci. U.S.A. 79:4575-4579(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-Human;
MEDLINE-84146798; PubMed-6142531;
Shen L.-P., Rutter W.J.;
"Sequence of the human somatostatin I gene.";
Science 224:168-171(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AA.
                                                                                 removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                   use by non-profit institutions as lon modified and this statement is not removentlies requires a license agreement (S or send an email to licensee(sb-stb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                          12; RIIDSI.
IPRO04250; Somatostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-M.fascicularis;
MEDLINE-88144503; PubMed-2894033;
Travis G.H., Sutcliffe J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-Human;
MEDLINE-83014931; PubMed-6126875;
                                                                                                                                                                     EMBL; M25903; AAA49339.1; -.
                                                                                                                                                                                                               CAA23878.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                           CAA23877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606, 9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens (Human),
                                                                                                                                                                                                                                     RIIDS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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P01166;
                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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Matches
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SMS_HUMAN
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                                                                                                                                                                                                                                                                                    Score 83.5; DB 1; Length 116;
Pred. No. 0.013;
L4: Mismatches 25; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        5 QIHCALALLGLALAICSQGAA-SQPDLDLASRRLLQRALAAALPHRSGVSERWRTFYPNC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [4]
SEQUENCE OF 101-114.
MEDLINE-81264223; PubMed-6114953;
Andrews P.C., Dixon J.E.; of a peptide hormone predicted from a mRNA "Isolation and structure of a peptide hormone predicted from a mRNA second sandtostatin from the catfish pancreas.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostarlophysi; Siluriformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-82265698; PubMed-6179939; Minth C.D., Taylor W.L., Magazin M.D., Tavlanini M.A., Collier K.J. Wetth H.L., Dixon J.E.; The structure of cloned DNA complementary to catfish pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 82-114 FROM N.A.
MEDLINE-82082515; PubMed-6171821;
TAYLOR W.L.; COllier K.J., Deschenes R.J., Weith H.L., Dixon J.
"Sequence analysis of a cDNA coding for a pancreatic precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor [Contains: Somatostatin-14 (SS-14)].
atus. Channel catfish).
                                                                                                                                                                                                                                   105 116
116 AA; 12675 MW; 8A5BB9BDA8A291BA CRC64;
                                                                                                                    of basic residues; Hormone; Signal
24 BY SIMILARITY.
88 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOMATOSTATIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roc. Natl. Acad. Sci. U.S.A. 78:6694-6698(1981).
                                                                                                                                                                                         SOMATOSTATIN-28.
                                                                                                                                                                                                               SOMATOSTATIN-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; , 114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update
                                                                                                                                                                                                                                                                                                                                     14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #EDLINE=85303576; PubMed=2863931;
lixon J.E., Andrews P.C.;
Somatostatins of the channel catfish.";
dv. Exp. Med. Biol. 188:19-29(1985).
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            natostatin-14 messenger RNA.";
Biol. Chem. 257:10372-10377(1982).
                                                                            InterPro; IPR004250; Somatostatin.
Pfam; PF03002; Somatostatin: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- TISSUE SPECIFICITY: PANCREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 PCLRWRPRKVKGPQLKAKEDLER 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56 -- LLSEPSQTENEALES-EDLSR 75
                                                                                                                                                                                                                                                                                         18.6%;
illarity 37.3%;
Conservative 14
                                       EMBL; X60191; CAA42747.1; -. PIR; S20630; S20630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ctalurus
                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
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                                                                                                                             Cleavage on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMS1_ICTPU
P01171:
                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                           EPTIDE
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ICTPU
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us-09-727-739b-17.rsp

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                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular cloning of the cDNAs and distribution of the mRNAs encoding two somatostatin precursors in the African lungfish Protopterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage on pair of basic residues; Hormone; Multigene family; Signal.
SIGNAL 1 24
                                                                                                                                                                                                                                                                    Hormone; Multigene family; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frabucchi M., Tostivint H., Lihrmann I., Jegou S., Vallarino M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurol. 410:643-652(1999).
10N: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                   Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Somatostatin I precursor (PSSI) [Contains: Somatostatin-27;
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                                                                                     use by non-profit institute. There are no rest modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOMATOSTATIN-27 (POTENTIAL). SOMATOSTATIN-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRVSQIHCALALLGLALAICSQGAA-SQPDLDLASRRLLQRALAAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY.
349756FEB4ABE213 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eu
Dipnoi, Lepidosireniformes, Protopteridae, Protopterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Somatostatin-14).
Protopterus annectens (African lungfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Secreted.
SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
                   BELONGS TO THE SOMATOSTATIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                    0.079;
                                                                                                                                                                                                                                                                                                                         SOMATOSTATIN-14.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.07
8; Mismatches
                                                                                                                                                                                                                                                                                 BY SIMILARITY
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                                                                                                                                                                                                                          Interpro, IPR004250; Somatostatin. Pfam; PF03002; Somatostatin; 1. Cleavage on pair of basic.residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004250; Somatostatin.
Pfam; PF03002; Somatostatin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain;
MEDLINE-99326690; PubMed-10398054;
  SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF126243; AAD39138.1; -.
                                                                                                                                                                                                                                                                                                                                                            12691 MW;
                                                                                                                                                                                                                                                                                                                                                                                               17.0%;
                                                                                                                                                                                                             EMBL; U68136; AAC60093.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 47.8 tes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                          104 J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I_TaxID=7888;
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Q9W7F0;
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIHCALALLGLALAI-CSQGAASQPDLDLASRRLLQRALAAALPHRSGVSERWRTFYPNC 63
                                                                                                                                                                                                                                                                                                                                          Pfam; PF03002; Somatostatin; 1.
Cleavage on pair of basic residues; Hormone; Signal; Pharmaceutical:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ry H., Chartrel N., Conlon J.M.;
Lation of [Pro2,Met13]somatostatin-14 and somatostatin-14 from
brain reveals the existence of a somatostatin gene family in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rana ridibunda (Laughing frog) (Marsh frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Barzachia; Anura, Neobatrachia; Ranoldea; Ranidae, Rana
NCBI_TaxID=8406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
sor (PSS1) [Contains: Somatostatin-14 (S-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tostivint H., Lihrmann I., Bucharles C., Vieau D., Coulouarn Y., Fournier A., Conlon J.M., Vaudry H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun. 188:477-482(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Occurrence of two sometostatin variants in the frog brain: characterization of the CDNAs, distribution of the mRNAs, ard receptor-binding affinities of the peptides "; Proc. Natl. Acad. Sci. U.S.A. 93:12605-12610(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
12735 MW; AB49BB89DC9DD8DA CRC64;
peptide tumors.
                   BELONGS TO THE SOMATOSTATIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 79.5; DB 1; 1
Pred. No. 0.037;
1; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                SOMATOSTATIN-28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 AA.
                                                                                                                                                                                                                                                                                                                InterPro; IPR004250; Somatostatin.
Pfam; PF03002: Somatostatin. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97057290; Pubmed-8901629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93038702; PubMed=1358069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LLSEPNQTENDALE-PEDLSQ 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
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16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.7%;
ilarity 34.9%;
Conservative 1
                                                                                                                                                                                                         EMBL; J00306; AAA60566.1;
EMBL; M19318; AAA36908.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somatostatin 1 precursor (SSS1)].
                                                                                                                                                                                                                                                                                 HGNC:11329; SST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 1
116 AA;
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                                                                                                                                                                                                                                              PIR; A43614; RIHUS1
PIR; A28968; A28968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                   SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09PSI8;
                                                                                                                                                                                                                                                                             Genew; Hunc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fournier A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMS1_RANRI
P87384; 091
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125 AA.

BY SIMILARITY.
BOCEF1E603FEAF09 CRC64;

104 115 B

DISULFID

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- MISCELLANEOUS: SOMATOSTATIN II MAY HAVE A DIFFERENT DEGREE OF ACTIVITY OR A DIFFERENT TYPE OF TARGET CELL FROM SOMATOSTATIN I. SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 IHCALALLGLALAICSQGAASQ-----PDLDLASRR--LLQRALAAALPHRSGVSER 55
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                                                                                                                                                                 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Actinopterygii: Neopterygii; Teleostei; Euteleostei; Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Acanthomorpha: Paracanthopterygii; Lophiiformes; Lophiidae; Lophius. Next. TaxID-8073; Paracanthopterygii; Lophiiformes; Lophiidae; Lophius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Somatostatin; 1.
Sair of basic residues; Hormone; Signal; Hydroxylation;
                                                                                                                                                 [Tyr7,Gly10]somatostatin-14]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE, AND HYDROXYLATION.
MEDLINE-B738104: PubMed-288752;
Andrews P.C. Nichols R. Dixon J.E.;
"Post-translational processing of preprosomatostatin-II examined using fast atom bombardment mass spectrometry.";
J. Biol. Chem. 262-12692-1269(1987).
-- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-81052423; Pubmed-6107860; Plotet R., Rutter W.J.; Pubart P.M., Crawford R., Shen L., Plotet R., Rutter W.J.; Ploning and sequence analysis of cDNAs encoding two distinct somatostatin precursors found in the endocrine pancreas of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.4%; Score 69.5; DB 1; Length 125; Best Local Similarity 36.1%; Pred. No. 0.53; Matches 22; Conservative 7; Mismatches 17; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [TYR7,GLY10]SOMATOSTATIN-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROXYLATION.

DV -> TG (IN REF. 1).

G -> E (IN REF. 1).

5E14605D7B9A46FE CRC64;
01170; 091066;
21-70L-1986 (Rel. 01, Created)
01-0CT-1999 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
16-0CT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 AA; 14052 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMBL; V00641; CAA23987.1; -.
                                                                                                                                             Somatostatin II precursor
Lophius americanus (Americ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 288:137-141(1980).
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - SUBCELLULAR
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P26917;
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STRIN-ILE de France;
MEDLINE-99094691; Pubmed-9880082;
Bruneau G., Tillet Y.;
"Localization of the preprosomatostatin-mRNA by in situ hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 QIHCALALIGLALAICS-QGAASQPDLDLASRRLLQRALAAALPHRSGVSERWRTFYPNC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 RLQCALAALSIVLALGGVTGAPSDPRL----RQFLQKSLAAA----AGKQELAKYFLAE- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Somatostatin precursor [Contains: Somatostatin-14]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Cranlata; Verrebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Captinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the ewe hypothalamus.";
bides 19:1749-1758(1998).
FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
                                                                Query Match
16.8%; Score 75.5; DB 1; Length 115;
Best Local Similarity 48.8%; Pred. No. 0.1;
Matches 20; Conservative 4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 15.4%; Score 69.5; DB 1; Length 116; Best Local Similarity 33.7%; Pred. No. 0.49; Matches 28; Conservative 13; Mismatches 29; Indels 13
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C18F17E31A3718DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                              5 QIHCALALLGLALAICSQGAASQPDLDLASRRLLQRALAAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                               .PRT; 116 AA.
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entities requires a license agreement (
or send an email to license@isb-sib.ch)
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116 AA; 12689 MW;
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CBI_TaxID=9940

SMS_SHEEP 046688;

RESULT 9 SMS_SHEEP

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MEDLINE—92348367; PubMed-1379225;
Sessa W.C., Harrison J.K., Barber C.M., Zeng D., Durieux M.E.,
D'Angelo D.D., Lynch K.R., Peach M.J.;
"Molecular cloning and expression of a cDNA encoding endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 LALAICSQGAASQPD---LDLASRRLLQRALAAALPHRSGVSERWRTFYPNCPCLRWRPR 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----RTQIPPSGLLPFRPK 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000003; AAB92468.1; -
InterPro; IPR002104; Phage_integrase.
Pfam; PF00589; Phage_integrase; 1.
Hypothetical protein; DNA recombination; DNA integration; Plasmid; Transposable element.
SEQUENCE 314 AA; 36310 MW; 9D33FBESAAE95068 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JRP-1993 (Rel. 25, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nitric-oxide synthase, endothelial (EC 1.14.13.39) (EC-NOS) (NOS, III) (NOSIII) (Endothelial NOS) (CONStitutive NOS) (CNOS).
                                                      reiberg C.A., Fellay R.; Bairoch A., Broughton W.J., Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Indels 13;
                                                                                                               symbiosis between Rhizobium and legumes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92335295; PubMed-1378626;
Lamas S., Marsden P.A., Li G.K., Tempst P., Michel T.;
"Endothelial nitric oxide synthase: molecular cloning and
caracterization of a distinct constitutive enzyme isoform.";
Proc. Natl. Acad. Sci. U.S.A. 89:6348-6352(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB.1; Length 314;
                                                                                                               "Molecular basis of symbiosis between Rhizobium and legu
Nature 387:394-401(1997)
-I- SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 15.0%; Score 67.5; Di Local Similarity 33.3%; Pred. No. 2.3; es 25; Conservative 11; Mismatches
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   SEQUENCE FROM N.A.
MEDLINE-97305956; Pubmed-9163424;
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99 RAR-PYLYSKEDIGR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOS3_BOVIN
P29473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
NOS3_BOVIN
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01-AUG-1992 (Rel: 23, Created)
01-AUG-1992 (Rel: 23, Last sequence update)
16-OCT-2001 (Rel: 40, Last annotation update)
Somatostatin precursor [Contains: Somatostatin-28; Somatostatin-14].
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-HOLStein;
MEDILINE-991870: PubMed-10100681;
FULU L.M., Kazmer G.W., Strausbaugh L., Zinn S.A.;
"Cloning and characterization of the bovine somatostatin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Anim. Sci. 77:492-493(1999).
-1- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
-1- SUBCELLUIAR LOCATION: Secreted.
-1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                 Saunders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 68.5; DB 1; Length 116;
Pred. No. 0.64;
7; Mismatches 11; Indels 5
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                                                                                                                                                                                                                                                                                                                                               MEDLINE-88288237; PubMed-2899837;
Su C.J., White J.W., Li W.H., Luo C.C., Frazier M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Somatostatin; 1.
1r of basic residues; Hormone; Signal.
1 24 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Structure and evolution of somatostatin genes."; Mol. Endocrinol. 2:209-216(1988).
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01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Putative integrase/recombinase Y4RB.
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SOMATOSTATIN-14.
BY SIMILARITY.
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llarity 45.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004250;
Pfam; PF03002; Somato
                                                                                                                                                    taurus (Bovine).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 AA;
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Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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P55635;
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AC P55635
DT 01-NOV-
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DE PUTATIV
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-> I (IN REF. 3).
-> I (IN REF. 3).
HPPLEMPAAL. -> GAPHTGVVRGP (IN REF. 3).
-> Y (IN REF. 3).
-> P (IN REF. 3).
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PAN (PYRINDINE PART) (BY SIMILARITY
PAD (ADP PART) (BY SIMILARITY).
PAD (FLAVIN PART) (BY SIMILARITY).
NADP (RIBOSE PART) (BY SIMILARITY).
NADP (ADP PART) (BY SIMILARITY).
MADP (ADP PART)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               es, NADP; FAD; FWN; Calmodulin-binding; Myristate;
Palmitates; Phosphorylation; Calcium-binding; Heme;
binding; Multigene family; 3D-structure.
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-> V (IN REF. 3).
-> LV (IN REF. 3).
-> H (IN REF. 3).
-> H (IN REF. 3).
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PHOSPHORYLATION (BY PKA).
modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
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PALMITATE.
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709; FNPLCyt_redctse.
094; Flavdoxin_like.
226; Flavodoxin.
030; NO_synthase.
433; Oxred_FAD/NAD(P).
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4 <u>%</u>
                                                                                                                      M99057; AAA30667:1; -. M89952; AAA30494:1; -. M95674; AAA30669:1; -.
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Oxidoreductase; NADP; FAD;
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INIT_MET
BINDING
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CONFLICT
SEQUENCE
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NP_BIND
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2008;
2008;
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Raman C.S., Li H., Martasek P., Babu B.R., Griffith O.W., Southan G.,
Raman C.S., Li H., Martasek P., Babu B.R., Griffith O.W., Southan G.,
Masters B.S.S., Poulos T.L.; Babu B.R., Griffith O.W., Southan G.,
Implications for 1soform-selective inhibitor design derived from the
binding mode of bulky isothioureas to the heme domain of endothelial
J. Biol. Chem. 276.26486-26491(2001)
II. FUNCTION: PRODOCES MITRIC OXIDE (NO) WHICH IS IMPLICATED IN
VASCULAR SMOOTH MUSCLE RELAXATION THROUGH A CGMP-MEDIATED SIGNAL
FRANSDUCTION PATHWAY. NO MEDIATES VASCULAR ENDOTHELIAL GROWTH
FRACTOR (VEGF)-INDUCED ANGIOGENERIS IN CORONARY VESSELS AND
PROMOTES BLOOD CLOTTING THROUGH THE ACTIVATION OF FLATELETS.
II. CATALITY: L.axginine + N NADPH + M O(2) = citrulline +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20503854; PubMed-11051558;
Li H., Raman C.S., Martasek P., Kral V., Masters B.S.S., Poulos T.L.;
Mapping the active site polarity in structures of endothelial
nitric oxide synthase heme domain complexed with isothioureas.";
J. Inorg. Blochem. 81:133-139(2000).
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                                                                                                                                                                                                                                                                                                                                                          Robinson L.J., Michel T., "Mutagenesis of palmitoylation sites in endothelial nitric oxide synthase identifies a novel motif for dual acylation and subcellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 66-481.
MEDLINE-99091052; PubMed-9975848;
Raman C.S., Li H., Martasek P., Kral V., Masters B.S.S., Poulos T.L.;
"Crystal structure of constitutive endothelial nitric oxide synthase:
a paradigm for pterin function involving a novel metal center.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
MEDILINE-1552923; PubMed=11695891;
Raman C.S., Li H., Martasek P., Southan G., Masters B.S.S.,
Poulos T.L.; Crystal structure of nitric oxide synthase bound to nitro indazole
reveals a novel inactivation mechanism.";
Michemistry 40:13448-13455(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.93 ANGSTROMS).
MEDLINE-21220525; Pubmad=11331003;
LLH H., Raman C.S., Martasek P., Masters B.S.S., Poulos T.L.;
"CLYStallographic studies on endothelial nitric oxide synthase complexed with nitric oxide and mechanism-based inhibitors.";
Blochemistry 40:5399-5406(2001).
                                                                                                            MEDLINE-93231982; PubMed-7682550; Busconi L., Michel T., Endothellal nitric oxide synthase: N-terminal myristoylation determines subcellular localization."; Jaioi. Chem. 268:8410-8413(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENZYME REGULATION: STIMULATED BY CALCIUM/CALMODULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 92:11776-11780(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.86 ANGSTROMS) OF 66-481.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO THE NOS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRYSTALLOGRAPHY (1.93 ANGSTROMS).
   oxide synthase.";
.. Chem. 267:15274-15276(1992).
                                                                                                                                                                                                                                                                                                                                 MEDLINE-96102197; PubMed-8524847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nitric oxide + N NADP(+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 95:939-950(1998).
                                                                                       MYRISTOYLATION
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   nitric ox
J. Biol. (
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Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-NRRL Y-12624;
COSTARAIN-OFF T.D.;
COSTARAZO M.C., FOX T.D.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: REQUIRED FOR EXPRESSION OF THE MITOCHONDRIAL GENE FOR CYTOCHROME, C OXIDASE SUBDNIT III (COX1). PET122 SEEMS TO WORKS BY DIRECTLY INTERACTING WITH THE SMALL RIBOSOMAL SUBDNIT TO PROMOTE TRANSLATION INITIATION ON THE COXIII MRNA (BY STMILARITY).
-I- SUBCELLULAR LOCATION: MITOCHONDRIAL; INNER MEMBRANE ASSOCIATED (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .. 108 MGLGRGTSASASAEAQAVEFELRRYKVEAFARGTMHSTALSEKWKVFLQEMDTLPGQPPL 167
                                                         Gaps
                                                                                            8 CALALLGLALAIC-SQGAAS---QPDLDLASRRILQRALAAALPHRSGVSERWRTFYPNC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                    ------SRAPAPATPHAPDHSPA-----PNS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF026394; AAB82600.1; -.
Translation regulation; Activator; Transit peptide; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces bayanus (Yeast) (Saccharomyces uvarum).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                         20;
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9
             Length 1204;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.7%; Score 66; DB 1; Length 260; 27.0%; Pred. No. 2.8; Live 10; Mismatches 30; Indels
                                                       25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ET122 PROTEIN.
80AFEC2A7238262F CRC64;
                Score 67; DB 1;
Pred. No. 10;
4; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
PET122 protein, mitochondrial precursor.
                                                                                                                                                                                                                                                                                                                      260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                      · PRT;
                                                                                                                      14 CGLG-LGLGLCGKQGPASPAPEP-
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260 AA; 29016 MW;
             14.9%;
           Query Match
Best Local Similarity 35.5
Matches 27; Conservative
                                                                                                                                                                                                Conservative
                                                                                                                                                                         64 PCLRWRPRKVKGPQLK 79
                                                                                                                                                                                                                                                                                                                    STANDARD;
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17; Conserv
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TRANSIT
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P01167;
21-JUL-1986 (
21-JUL-1986 (
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013374;
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PT22_SACBA
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SMS_MOUSE
ID SMS_M
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FOT 21-JU
DT 21-JU
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Matches
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Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                      MEDLINE-85006903; PubMed-6148343;
Tavianini M.A., Hayes T.E., Magazin M.D., Minth C.D., Dixon J.E.
"Isolation, characterization, and DNA sequence of the rat
Somatostatin gene."
J. Biol. Chem. 259:11798-11803(1984).
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"Somatostatin-28 encoded in a cloned cDNA obtained from a rat
medullary thyroid carcinoma.";
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MEDLINE—86070564; PubMed—22891188;.
MEDRINE—86070564; PubMed—22891188;.
"A new prosomatostatin-derived peptide reveals a pattern for probromone cleavage at monobasic sites.";
Schence 238:1126-1129(1987).
16-OCT-2001 (Rel. 40, Last annotation update)
Somatostatin precursor (Contains: Antrin; Somatostatin-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITINE-83238516; PubMed-6134734;
Argos P., Taylor W.L., Minth C.D., Dixon J.E.;
"Nucleotide and amino acid sequence comparisons of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE-85303584, PubMed-2863939,
Goodman R.H., Montaniny M.R., Low M.J., Hat
"Blosynthesis of rat preprosomatostatin:",
Adv. Exp. Med. Blol. 188:31-47(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 258:5570-5573(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=82120034; PubMed=6120163;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-83213516; PubMed-6133871;
                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE OF 38-116 FROM N.A.
                                                                                                         (Mouse), and
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                        Somatostatin precui
Somatostatin-14).
SST OR SMST.
Mus musculus (Mous
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Search completed: March 21, 2003, 11:38:40 Job time : 13.3348 secs

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Sometostatin precursor - chicken
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Accession: 320630
R; Nata, K; Kobayashi, T; Karahashi, K; Kato, S; Yamamoto, H; Yonekura, H; Oka submitted to the EMBL Data Library, June 1991
A; Description: Nucleoctide sequence determination of chicken somatostatin precursor A; Reference number: $20630
A; Accession: $20630
A; Accession: $20630
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-116 < NAT>
A; Cross references: EMBL:X60191; NID:962985; PIDN:CAA42747.1; PID:962986
C; Superfamily: somatostatin
                                                                                                                                                                                                                                                                                                                                                                                                                       Sometostatin II precursor - rainbow trout
C.Species: 0ncorhynchus mykiss (rainbow trout)
C.Species: 0ncorhynchus mykiss (rainbow trout)
C.Accession: 151064
R.Moore, C.A.; Kittilson, J.D.; Dahl, S.K.; Sheridan, M.A.
Gen. Comp. Endocrinol. 98, 253-261, 1995
A.Fitle: Isolation and characterization of a cDNA encoding for preprosomatostatin c
A.Feference number: 151064; MUID:95354921; PMID:7628684
A.Status: preliminary; translated from GP/EMBL/DDBJ
A.Festius: preliminary; translated from GP/EMBL/DDBJ
A.Festius: preliminary; translated from GP/EMBL/DDBJ
A.Festius: 1-115 <a href="mailto:cNoo">c.Comp. CNOO</a>
A.Coss-references: EMBL:U32471; NID:9975344; PIDN:AAC59695.1; PID:9975345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 77.2%; Score 347.5; DB 2; Length 11: Best Local Similarity 85.7%; Pred. No. 9.6e-32; Matches 72; Conservative 2; Mismatches 7; Indels
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                                                                                         B85723
S16359
C75625
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somatostatin II pr
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probable GntR-fami
probable ATP/GTP-b
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                 March 21, 2003, 11:38:56; Search time 18.4549 Seconds (without alignments) 447.986 Million cell updates
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                   5.1.4_p5_4578
Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                    283224 seqs, 96134422 residues
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                 GenCore version Copyright (c) 1993 - 2003
                                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5.
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Maximum Match 100%
Listing first 45 su
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                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0 seq length: 2000000000
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Maximum DB
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5 QIHCALALLGLALAICSQGAA-SQPDLDLASRRLLQRALAAALPHRSGVSERWRTFYPNC

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A) Description: inhibits the secretion of a number of peptide hormones, including soma C; Superfamily: somatostatin
C; Keywords: hormone; hypothalamus; neuropeptide
C; Keywords: hormone; hypothalamus; neuropeptide
F;1-34.70omain: signal sequence #status predicted <FRO>
F;25-88.70omain: somatostatin-28 #status predicted <ARO>
F;89-116/Product: somatostatin-14 #status predicted <ALO+
F;103-116/Product: somatostatin-14 #status predicted <ALO+
F;105-116/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          le: Site-specific mutagenesis identifies amino acid residues critical in prohorm
erence number: S09381; MUID:90059875; PMID:2573512
                                                                                                                                                                                                                                                                                                                                      Alternate names: preprosomatostatin
Contains: somatostatin 14 (SS-14); somatostatin 28 (SS-28)
Species: Homo sapiens (man)
Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 18-Jun-1999
Accession: A43614; A01430; S09381; S50024
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                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ul source: pancreatic somatostatinoma
Bolleau (6; Zollinger, L.; Nault, C.; Rholam, M.; Cohen, P.
111.2916, 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: DNA
Residues: 1-116 <SH2>
Cross-references: GB:J00306; NID:9338287; PIDN:AAA60566.1; PID:9338288
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Best Local Similarity 46.7%; Pred. No. 0.078;
Matches 21; Conservative 8; Mismatches 11; Indels
                                                                                                                                1 MRVSQIHCALALLGLALAICS-QGAASQPDLDLASRRLLQRALAA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shen, L.P.; Pictet, R.L.; Rutter, W.J.; Croc. Natl. Acad. Sci. U.S.A. 79, 4575-4579, 1982. Croc. Natl.: Acad. Sci. U.S.A. 79, 4575-4579, 1982. Filtle: Human somatostatin I: sequence of the cDNA. Reference number: A01430; MUID:83014931; PMID:6126875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecule type: mRNA
fessidues: 88-108 < COM>
Codum, L. Johnsen, A.H.
Jochem. J. 303, 263-268, 1994
Aritle: Human seminal plasma contains somatostatin-64
Reference number: S50024; MUID:95031969; PMID:7945250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shen, L.P.; Rutter, W.J.
Hence 224, 168-171, 1984
Title: Sequence of the human somatostatin I gene.
Reference number: A43614; MUID:84146798; PMID:6142531
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sidues: 53-62;67-82 <ODU>
mment: Somatostatin inhibits the release of
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Introns: 46/3
Function:
                                                                                                                                                                                                                                                                                                             somatostatin I precursor · human
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Residues: 1-116 <SHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: A43614
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                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Ictalurus punctatus (channel catfish)
C;Date: 30-Juni1980 Asequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C;Date: 30-Juni1980 Asequence_revision 31-Dec-1993 #text_change 18-Jun-1999
C;Accession: S00292; A93897; A92344; A01435
R;Minth, C.D.; Taylor, W.L.; Magazin, M.; Tavianini, M.A.; Collier, K.; Weith, H.L.; Dix J. Bhil. Chem. 257, 10372-10377, 1982
J. Bhil. Chem. 257, 10372-10377, 1982
A;Title: The structure of cloned DNA complementary to catfish pancreatic somatostatin-14
A;Reference number: S00292; MUID:82265698; PMID:6179939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: EMBL:V00607; NID:964017; PIDN:CAA23877.1; PID:964018
roc. Natl. Acad. Sci. U.S.A. 78, 6694-6698, 1981
intitle: Sequence analysis of a.cDNA coding for a pancreatic precursor to somatostatin.
Reference number: A93897; MUID:82082515; PMID:6171821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 256, 8267-8270, 1981
Title: Isolation and structure of a peptide hormone predicted from a mRNA sequence. A
Reference number: A92334; MUID:81264223; PMID:6114953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preprosomatostatin SS-14 - channel catfish
C:Species: Ictalurus punctatus (channel catfish)
C:Date: 13-8ep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
       :| | : |
---AGKQELAKYFLAE- 55
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A;Residues: 1114 - 011X>
A;Cross references: GB:M55903; NID:g213339; PIDN:AAA49339.1; PID:g213340
C;Superfamily: somatostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.9%; Score 80.5; DB 1; Length 114; 46.7%; Pred. No. 0.078;
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Adv. Exp. Med. Biol. 188, 19-29, 1985
Adv. Exp. Med. Biol. 188, 19-29, 1985
A;Title: Somatostatins of the channel catfish.
A;Reference number: 150798; MUID:85303576; PMID:2863931
A;Stecession: 150798
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                somatostatin-14 precursor - channel catfish
   S RIQCALALLSIALAVGTVSAAPSDPRL-
                                                                                               64 PCLRWRPRKVKGPQLKAKEDLER 86
                                                                                                                                       ; Dixon, J.E.
256, 8267-8270, 1981
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sidues: 82-108 <TAY>
oss-references: GB:J00944
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Residues: 101-114 <AND
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.: Residues: 1-114 <MIN>
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64 PCLRWRPRKVKGPQLKAKEDLER 86

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A; Molecule type: protein
A; Mesideus: 98-125 <5ET-7
A; Andrews, P.C.; Nichols, R.; Dixon, J.E.
A; Andrews, P.C.; Com. 267, 12692-12699, 11987
A; Title: Post-translational processing of preprosomatostatin-II examined using fast
A; Reference number: A27376; MUID:87308304; PMID:2887572
                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1.125 < HOB>
A; Residues: 1.25 < CHOB>
A; Cross-references: GB:V00641; GB:J00947; GB:M23199; NID:g64030; PIDN:CAA23987.1; P
A; Experimental source: islet tissue (endocrine pancreas)
A; Experimental source: islet tissue (sendocrine pancreas)
Broc. Natl. Acad. Sci. U.S.A. 82, 277-281, 1985
A; Title: Processing of an anglerfish somatostatin precursor to a hydroxylysine-cont
A; Reference number: A94038; MUID:85113184; PMID:2857489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;25-97/Domain: propeptide #status experimental <PRO>
F;97-125/Product: somatostatin II #status experimental <MAT>
F;57-Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status expe F;114-125/Disulfide bonds: #status experimental F;110/Modified site: hydroxylysine (Lys) #status experimental
                                                                     C; Species: Lophius americanus (American goosefish)
C; Date: 31-Mar-1981 # sequence_revision 31-Mar-1981 # text_change 28-May-1999
C; Date: 31-Mar-1981 # sequence_revision 31-Mar-1981 # text_change 28-May-1999
C; Accession: B92236; A94038; A27376; A01444; A21881; A3236
R; Hobart, P.; Crawford, R.; Shen, L.; Pictet, R.; Rutter, W.J.
Nature 288, 137-141, 1980
A; Title: Cloning and sequence analysis of cDNAs encoding two distinct somatostatin A; Reference number: A93236; MUID:81052423; PMID:6107860
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A;Title: Structure and evolution of somatostatin genes.
A;Reference number: A40929; MUID:88288237; PMID:2899837
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N;Contains: somatostatin 14 (SS-14); somatostatin 28 (SS-28)
C:Species: Bos primigenius taurus (catile)
C:Date: 06-Mar-1992 #sequence_revision 31-Jan-1997 #text_change 18-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M31217; NID:g163636; PIDN:AAA30744.1; PID:g1636337 A;Note: the authors translated the codon ATT for residue 65 as Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.4%; Score 69.5; DB 1; Length 125; 36.1%; Pred. No. 1.5; ive 7; Mismatches 17; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    authors translated the codon ATT for residue 65 as Asn Somatostatin inhibits the release of somatotropin.
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1-24/Domain: signal sequence #status experimental <SIG>
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Residues: 1-76,'DV',79-89,'G',91-125 <AND>
Superfamily: somatostatin
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A; Molecule type: mRNA
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JG614 H.; Lihrmann, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; Cd. Matl. Acad. Sci. U.S.A. 93, 12605-12610, 1996

JTitle: Occurrence of two somatostatin variants in the frog brain: Characterization of Reference number: JG6166; MUID:97057290; PMID:8901629
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Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone.
                                                                                                                                                                                                                                                                                                                                                      fravis, G.H.; Sutcliffe, J.G.
roc. Natl. Acad. Sci. U.S.A. 85, 1696-1700, 1988
fritle: Phenol emulsion-enhanced DNA-driven subtractive cDNA cloning: isolation
freference number: A28968; MUID:88144503; PMID:2894033
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C;Species: Rana ridibunda (laughing frog)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999
                                                                                                                                                                                    N;Alternate names: preprosomatostatin
N;Contains: somatostatin 14 (SS-14); somatostatin 28 (SS-28)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 30-Jun-1989 #sequence_revision 31-Jan-1997 #text_change 18-Jun-1999
C;Accession: A28968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Croment: Sometostatin Inhibits the release of sometotropin. Subjectantly: sometostatin Inhibits the release of sometotropin.
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; Pred. No. 0.1;
13; Mismatches 28; Indels 13;
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Pred. No. 0.22;
8; Mismatches 11; Indels
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                                                                                                                                                                  somatostatin I precursor - crab-eating macaque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 PCLRWRPRKVKGPQLKAKEDLER 86
   -- LLSEPNOTENDALE-PEDLSQ 75
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47.8%;
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Best Local Similarity 47.8
Matches 22; Conservative
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C:Keywords: brain; hormone
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Matches
   26
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Residues: 1-120 <STO>
Cross-references: GB:AE004744; GB:AE004091; NID:99949317; PIDN:AAG06591.1; GSPDB:GN
Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I nitric oxide synthase: molecular cloning and characterization of
A46033; MUID:92335295; PMID:1378626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: F83244
Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchl, S.D.; Warrener, P.; Hickey, iman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein PA3203 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p-2000 #sequence_revision 15-5ep-2000 #text_change 31-Dec-2000 F83244
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRVSQIHCALALLGLALAICSQGA----ASQPDLDLASRRLLQRALAAALPHRSGVSER 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 MRPSAAHCLLLSLGASLALAEEPAPAPIPAAQPSITQATAE-LERRLVETERQRDELVSR 60
                                                                                                                                                                                                                                                                                                                                                                                       14 GLALAICSOGAASOPDIDIASRRILORALAA---ALPHRSGVSERWRIFYPNCPCLRWRP 70
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A;Residues: 1-1205 <LAM1>
A;Cross-references: GB:M89952; NID:g162976; PIDN:AAA30494.1; PID:g162977
A.Cross-references: EMBL.AF055848; PIDN:AAC62611.1
A.Experimental source: root culture
A.Note: accumulates during auxin-induced lateral root formation
C.Genetics:
A.Gene: AIR3
C.Superfamily: subtilisin-like proteinase ag12; subtilisin homology
                                                                                                                                                                                                                                           Ouery Match 15.1%; Score 68; DB 2; Length 758; Best Local Similarity 28.1%; Pred. No. 12; Matches 18; Conservative 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: Bos primigenius taurus (cattle)
C; Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_C
C; Accession: A38943; A46033; I45945; A42841; I45946; A3894
R; Lamas, S.; Marsden, P.A.; Li, G.K.; Tempst, P.; Michel,
submitted to GenBank, July 1992
A; Reference number: A38943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.9%; Score 67; DB Best Local Similarity 33.9%; Pred. No. 2.7; Matches 21; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tal source: aortic; Marsden, P.A.; L. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adman; S.; Yuan, Y.;
.; Lory, S.; Olson, M
Nature 406, 959-964,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: F83244.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 MR 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conserved hypothetical protein XF2472 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Accession: A82534
R;anonymous. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
Title: The genome sequence of the plant pathogen Xylella fastidiosa.
Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A. Rolecule type: DNA
A. Residues: 1435 calls.
A. Residues: 1435 calls.
A. Residues: 1435 calls.
A. Residues: 1435 calls.
A. Experimental source: strain 9a5c
A. Experimental source: strain 9a5c
A. Experimental source: strain 9a5c
B. Simpson, A.J. G.; Relinach, E.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Bas-Necto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A. Authors: Ferreira, V.C.A.; Ferro, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Jonqueira, M.L.; Kathajha, J.P.; Krieger, J.B.; Nartunae, E.E.; Laign chado, M.A.; Madelra, M.B.N.; Madelra, M.W.F.; Martino, C.L.; Marques, M.V.; Martins, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr.; V.B.; de Sa, R.G.; Santelli, R.V.; Sawasah A. Authors: da Silva, A.C.R.; da Silva, A.M.; Silva, Jr., W.A.; da Silva, A.M.; Glada, S.; Vettore, A.L.; Z. A. Reference number: A59328
A. Reference number: A59328
A. Reference number: A59328
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C;Species: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 03-Nov-2000
C;Accession: T51335
R;Neuteboom. L.W.; Nuy J.M.Y.; Kuyper, M.; Ciljdesdale, O.R.; Hooykaas, P.J.J.; van der A;Neuteboom. 29, 273-287, 1999
A;Title: Isolation and characterization of cDNA clones corresponding with mRNAs that acc A;Reterence number: 225377; MUID:99178779; PMID:10080694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VSQIHC-----ALALLGLALAICSQGAASQPDLDLASRRLLQRALAAAL 46
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                                                                                                                                                                                                           15.2%; Score 68.5; DB 1; Length 116; 45.2%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: Aquifex aeolicus N-ethylammeline chlorohydrolase
                                                                                                                                                                                                                                       Pred. No. 1.8;
7; Mismatches 11; Indels
                               F;25-88/Domain: propeptide #status predicted <PRO>
F;89-116/Product: somatostatin-28 #status predicted <N28>
F;103-116/Product: somatostatin-14 #status predicted <N14>
F;105-116/Disulfide bonds: #status predicted <N14>
                                                                                                                                                                                                                                                                                                                                           5 QIHCALALGLALAICS-QGAASQPDLDLASRRLLQRALAAA 45
                                                                                                                                                                                                                                                                                                                                                                                   S RIQCALAALSIVLALGGVTGAPSDPRL----RQFLQKSLAAA 42
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       predicted
   F;1-24/Domain: signal sequence #status
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A; Matchors; Martins, E.M.F.; Marsuk,
F.G.; Nunes, E.R.; Ollveira, M.A.
Rodrigues, V.; Rosa, A.J. de M.; de
A; Authors; de Silva, A.C.R.; da C':
M.; Tsuhako, W.; Rosa, A.C.R.; da C':
                                                                                                                                                                                                                                       Local Similarity 45.2
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A; Residues: 1-758 <NEU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tatus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: XF2472
                                                                                                                                                                                                           Query Match
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27; Indels

endothelial cells i, G.K.; Tempst, P.; Michel, 89, 6348-6352, 1992

2; Length 120;

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GB:AE002557; GB:AE002098; NID:g7227332; PIDN:AAF42400.1; PID:g7
pe: serogroup B, strain MCS8
iman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.;
Is, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajand
                                                                                                                                                     A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 224 A;Reference number: A81775; MUID:20222556; PMID:10761919
                                                                                                                                                                                                                                                                                                                                       GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CAB83652.1; PID:g7
e: serogroup A, strain 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Homo sapiens (man)
C.Date: .21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 GRDIVVCGDWNIAHQNIDLKNWKGNQKN-SGFLPEEREWIGKVIHKLGWTDMWRTLYPDV 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PVPLTKEQLYQQAMEEAAWHHMPHPSD-SERI 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 GLALAICSOGAASOPDLDLASRRLLORALAAALP-----HRSGVSERWRTFYPNC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRVSQIHCALALLGLALAICSQGAASQPDLDLASRRLLQRALAAA----LPHRSGVSERW 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wlemann, S. submitted to the Protein Sequence Database, December 1999
A.Reference number: 222516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Experimental source: adult testis; clone DKFZp434L061
C;Gentics:
A:Note: DKFZp434L061.1
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.8%; Score 66.5; DB 2; 29.0%; Pred. No. 14; vative 15; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66.5;
Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     March 21, 2003, 11:41:40
                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: NMB2082; NMA0348
C,Superfamily: exodeoxyribonuclease III
                                A; Experimental source: serogroup R; Parkhill, J.; Achtman, M.; Jame
                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <PAR>
A;Cross references: (B:ALJ62752;
A;Experimental source: serogroup)
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Best Local Similaritý 24.6%;
Matches 16; Conservative 1
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es 20; Conserv
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A; Residues: 1-571 <AAA>
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Job time : 20.4549 secs
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          ule type: mRNA
uses: 1.1205 < URS
references: GBL:M99057; NID:g163421; PIDN:AAA30667.1; PID:g163422
W.C.; Harrison, J.K.; Barber, C.M.; Zeng, D.; Durieux, M.E.; D'Angelo, D.D.; Ly
Chem. 267, 15274-15276, 1992
: Molecular cloning and expression of a cDNA encoding endothelial cell nitric oxi
ence number: A42841; MUID:92348367; PMID:1379225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  esidues: 1.99, "R',101-164,'I',166-317,'GA',320,'HTGVVRGP',339-454,'Y',456-458,'P',460
ross-references: GB.M95674; NID:g163426; PIDN:AA30669.1; PID:g163427
ross-references: aortic endothelial cells
ote: submitted to GenBank, August 1992
ote: GenBank entry BOVNOS, release 103.0, has a typographical error in the reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sidues: 1-51, NV, 53-99, RV, 101-147, WV, 149-164, II', 166-317, GA', 320; HTGVVRGP', 329-3
517-692, G', 694-740, AV, 742-753, NV, 755-799, NV', 801-803, SA', 806-856, VV', 858-906, LDV
perimental source: aortic endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iption: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH family: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct dats: blocked amino end; calmodulin binding; chromoprotein; FAD; flavoprotein; FMN 12/Region: calmodulin binding #stetus predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence extracted from NCBI backbone (NCBIP:109564); contains a number of typog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sun, L.; Smith H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve nome sequence of Neisseria meningitidis serogroup B strain MCS8. 881000; MUID:20175755; PMID:10710307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [imported] - Neisseria meningitidis (strain MC58 serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .; Saunders, N.J.; Heldelberg, J.; Jeffries, A.C.; Nelson, K.E.; Elsen, J. Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignanl, V.; Pizza, M. 809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05/Domain: flavodoxin homology <FLX>
lfled site: myristylated amino end (Gly) (in mature form) #status predicted
iffed site: aspartic acid (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                וסטב-1900 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
Accession: H81009; A82031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CALALLGLALAIC-SQGAAS---QPDLDLASRRILLQRALAAALPHRSGVSERWRTFYPNC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SRAPAPATPHAPDHSPA-----PNS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;186/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADPH-ferrihemoprotein reductase homology <FEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 67; DB 1; Length 1205;
Pred: No. 25;
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                                                                                                                                                                                                                                                                   preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 25;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tus: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 14.9%;
Local Similarity 35.5%;
les 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTLTRPPEGPKFPRVK 74
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Matches
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Length 571; Indels

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Indels 11; Gaps

Length 259;

BLOSUM62 Gapop 10.0 ,

Searched:

Database

Title: Perfect score: Sequence: Scoring table:

Run on:

pred. No. is the number of ress score greater than or equal to and is derived by analysis of

tion	nce 41361, A	63,	1,	3, A	'n	. 24 ,	42,	132,	132,	ce 132, App	ce 132, App	132,	132,	132,	132,	132,	132,	132,	11.4
Descrip	Seque	Seque	Sequen	Sedue	Sedue	Sequen	Sequer	Sednen	Sequen	Sequen	Sequer	Sequen	Sequen	Sequen	Sequen	Sequer	Seguer	Sequer	
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OI BD	10	10	6	10 US-09-766-396-3	12	6	6	σ	σ	6	6	6	6	0	6	6	6	6	c
Length	95	513	333	110	110	833	333	333	333	333	.333	333	333	333	333	333	333	333	223
Query Match	15.0	14.6	14.1	13.9	13.9	13.8	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	13.7	100
Score	67.5	65.5	63.5	62.5	62.5	62.	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	61.5	
Result No.	П	7	E	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	
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US-09-864-761-41361 65.5 14.6 513 10 US-09-884-751-41361 62.5 13.9 110 10 US-09-766-396-3 62.5 13.9 110 10 US-09-766-396-3 62.5 13.9 13.9 US-09-765-375-3 62.5 13.9 US-09-470-275-54 61.5 13.7 933 9 US-10-001-054-42	Score Match Length DB ID 67.5 15.0 95 10 US-09-864-761-41361 65.5 14.6 513 10 US-09-884-761-41361 63.5 14.1 333 9 US-09-984-271-131 62.5 13.9 110 10 US-09-76-396-396-3 62. 13.8 833 9 US-10-062-375-3 61.5 13.7 333 9 US-10-0154-42 61.5 13.7 333 9 US-10-001-564-42 81.5 13.7 833 9 US-10-0164-42 82.0 US-072-132 83.0 US-10-028-072-132 83.0 US-10-028-072-132	Score Match Length DB ID 67.5 15.0 95 10 US-09-864-761-41361 65.5 14.6 513 10 US-09-884-761-41361 62.5 14.1 333 9 US-09-766-396-3 62.5 13.9 110 10 US-09-766-396-3 62.5 13.9 110 12 US-09-766-396-3 62.5 13.9 10.1 2 US-09-76-375-3 61.5 13.7 333 9 US-10-001-054-42 61.5 13.7 333 9 US-10-0121-32 61.5 13.7 333 9 US-10-121-32	Score Match Length DB ID 67.5 14.6 513 10 US-09-864-761-41361 65.5 14.6 513 10 US-09-884-761-41361 62.5 13.9 110 10 US-09-766-396-3 62.5 13.9 110 10 US-09-766-396-3 62.13.8 833 9 US-00-470-276-54 61.5 13.7 333 9 US-10-018-072-132 61.5 13.7 333 9 US-10-0132-94-2 61.5 13.7 333 9 US-10-121-049-132	Score Match Length DB ID 67.5 15.0 95 10 US-09-864-76141361 65.5 14.6 513 10 US-09-864-76141361 62.5 14.1 333 9 US-09-844-271-131 62.5 13.9 110 10 US-09-765-396-3 62.5 13.9 110 10 US-09-765-396-3 62.5 13.9 13.9 US-09-770-276-54 61.5 13.7 333 9 US-10-01054-42 61.5 13.7 333 9 US-10-028-072-132 61.5 13.7 333 9 US-10-121-049-132 61.5 13.7 333 9 US-10-132-904-132	Score Match Length DB ID 67.5 15.0 95 10 US-09-864-761-41361 65.5 14.6 513 10 US-09-864-761-41361 65.5 14.1 333 9 US-09-766-396-3 62.5 13.9 110 10 US-09-766-396-3 62.5 13.9 110 12 US-09-766-396-3 61.5 13.7 333 9 US-10-010-054-4 61.5 13.7 333 9 US-10-10-28-072-132 61.5 13.7 333 9 US-10-121-049-132 61.5 13.7 333 9 US-10-121-049-132 61.5 13.7 333 9 US-10-131-904-132	Score Match Length DB ID 67.5 15.0 95 10 US-09-864-761-41361 63.5 14.6 313 10 US-09-864-761-41361 63.5 14.1 313 9 US-09-984-271-131 62.5 13.9 110 10 US-09-76-396-396-3 62. 13.9 110 10 US-09-76-396-396-3 61.5 13.7 333 9 US-10-010-54-42 61.5 13.7 333 9 US-10-010-54-42 61.5 13.7 333 9 US-10-123-904-132 61.5 13.7 333 9 US-10-123-904-132 61.5 13.7 333 9 US-10-123-904-132 61.5 13.7 333 9 US-10-132-904-132 61.5 13.7 333 9 US-10-132-904-132 61.5 13.7 333 9 US-10-132-904-132 61.5 13.7 333 9 US-10-176-918-132 61.5 13.7 333 9 US-10-176-918-132	Score Match Length DB ID 67.5 15.0 95 10 US-09-864-761-41361 67.5 14.6 513 10 US-09-864-761-41361 62.5 14.1 333 9 US-09-944-271-111 62.5 13.9 110 10 US-09-766-396-3 62.5 13.9 110 10 US-09-766-375-3 61.5 13.7 333 9 US-10-001-054-42 61.5 13.7 333 9 US-10-010-054-3 61.5 13.7 333 9 US-10-121-049-132 61.5 13.7 333 9 US-10-121-049-132 61.5 13.7 333 9 US-10-132-04-132 61.5 13.7 333 9 US-10-132-04-132 61.5 13.7 333 9 US-10-175-746-132 61.5 13.7 333 9 US-10-175-746-132 61.5 13.7 333 9 US-10-175-746-132 61.5 13.7 333 9 US-10-176-921-132 61.5 13.7 333 9 US-10-176-921-132	Score Match Length DB ID 67.5 15.0 95 10 US-09-864-761-41361 65.5 14.6 513 10 US-09-864-761-41361 65.5 14.1 313 9 US-09-766-396-396-396-396-396-396-396-396-396-3	Score Match Length DB ID 67.5 15.0 95 10 US-09-864-76141361 67.5 14.6 513 10 US-09-864-76141361 62.5 14.1 933 9 US-09-844-771-131 62.5 13.9 110 10 US-09-765-396-3 62.5 13.9 110 10 US-09-766-396-3 61.5 13.7 333 9 US-10-01-054-32 61.5 13.7 333 9 US-10-01-04-132 61.5 13.7 333 9 US-10-121-049-132 61.5 13.7 333 9 US-10-121-049-132 61.5 13.7 333 9 US-10-132-904-132 61.5 13.7 333 9 US-10-176-918-132 61.5 13.7 333 9 US-10-176-918-132	Score Match Length DB ID 67.5 15.0 95 10 US-09-864-761-41361 67.5 14.6 513 10 US-09-864-761-41361 62.5 14.6 513 10 US-09-864-771-111 62.5 13.9 110 10 US-09-766-396-3 62.5 13.9 110 10 US-09-766-396-3 61.5 13.7 333 9 US-10-028-072-132 61.5 13.7 333 9 US-10-121-049-132 61.5 13.7 333 9 US-10-121-049-132 61.5 13.7 333 9 US-10-175-746-132 61.5 13.7 333 9 US-10-175-746-132 61.5 13.7 333 9 US-10-176-921-132 61.5 13.7 333 9 US-10-176-921-132 61.5 13.7 333 9 US-10-176-921-132 61.5 13.7 333 9 US-10-137-865-132 61.5 13.7 333 9 US-10-137-865-132	Score Match Length DB ID 67.5 15.0 95 10 US-09-864.761.41361 65.5 14.6 513 10 US-09-864.761.41361 62.5 11.9 110 10 US-09-63.3745.63 62.5 11.9 110 10 US-09-76.396.3 62. 11.9 110 10 US-09-76.396.3 61.5 11.7 31.3 9 US-10-010.474.2 61.5 11.7 31.3 9 US-10-010.474.2 61.5 11.7 31.3 9 US-10-112.9 61.5 11.7 31.3 9 US-10-112.9 61.5 11.7 31.3 9 US-10-112.9 61.5 11.7 31.3 9 US-10-1176.918-112.2 61.5 11.7 31.7 31.7 31.7 31.7 31.7 31.7 31.7

PCT/US01/00666

NUMBER: PCT, 2001-01-30 000-09-27

US 60/236,359 24263.6

PCT/US01/00667

PCT/US01/00664 PCT/US01/00669

NUMBER:

-01 - 30

NUMBER:

LICATION NUMBER:

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US-09-766-396-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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EXPRESSED IN LUNG, SIGNAL = 2
EXPRESSED IN HELA, SIGNAL = 2
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GCALLISTER, THOMAN,
WILON CLONING, OVEREXPRESSION AND TI
WILON: BIOACTIVE HISTIDINE AMMONIA.
                                                                                                        NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.0%; Score 67.5; D
27.7%; Pred. No. 0.81
.ive 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/833,745
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,770
US 60/234,687
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Patent No. US20020052038A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.6%;
Best Local Similarity 38.2%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Rhizobium meliloti
US-09-833-745-63
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                                                                                                                                                                                                           ORGANISM: Homo sapiens
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Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID
SOFTWARE: Patent]
SEQ ID NO 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-09-833-745-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICA
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-RESULT 3 US-09-984-271-131

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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-984-271-131
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STREET: 10666 No. US20020013456A1th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 AICSQ-GAASQP-DLDLASRRLLQRALAAALPHRSGVSERWRTFY---PNCPCLRWR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 14.1%; Score 63.5; DB 9; Best Local Similarity 33.3%; Pred. No. 9.9; Matches 19; Conservative 6; Mismatches 19;
Rosen et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,396
FILING DATE: 18-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATION NUMBER: PCT/US99/15849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Henriksen, Steven J. TITLE OF INVENTION: CORTISTATIN:
                                                                                                            IOR APPLICATION NUMBER: 09/482, 273
IOR FILING DATE: 2000-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sutcliffe, Gregor J.
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Patent No. US20020013456A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flope
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ORGANISM: Homo sapiens
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489 LGDLHCEIRDOETLLMYQLQCQVLARASVLTRVLDLASRLDVLLALASAARDYGYSRPHY 548
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                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: A METHOD OF DETECTION OF ALTERATIONS IN MSHS FILE REPRENCE: 70015/74443C CURRENT APPLICATION NUMBER: US/09/470, 276 CURRENT FILING DATE: 1999-1.2-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9; Length 833; 42;
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10; Indels
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                                     8 CALALLGLALAICS-QGAASQPDLDLASRRLLQRALAAA 45
                                                                             2 CALAALCIVLALGGVTGAPSDPRL----ROFLQKSLAAA 36
                                                                                                                                                                                                                                              DANA-FARBER CANCER INSTITUTE, INC
  5; Mismatches
                                                                                                                                                                                   Sequence 54, Application US/09470276
Publication No. US20020187469A1
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MBER: PCT,
1998-07-02
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Best Local Similarity 27.5
Matches 30; Conservative
19; Conservative
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PRIOR FILING DATE: 1998-0
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SOFTWARE: Pate
SEQ ID NO 54
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  Matches
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                                                                                                                                                                                                                                                                               Match 13.9%; Score 62.5; DB 10; Local Similarity 48.7%; Pred. No. 3.7; les 19; Conservative 5; Mismatches 10;
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APPLICATION NUMBER: US/10/062,375
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                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID, NO: 3: US-09-766-396-3
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No. US20020133000A1
RAL INFORMATION:
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Best Local Similarity
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PCT/US99/05028 MBER: PCT/US98/18824 998-09-10 PCT/US99/08615 PCT/US99/12252 PCT/US99/20111 PCT/US99/28313 PCT/US99/28634 APPLICATION NUMBER: PCT/US99/00106 FILING DATE: 1999-01-05 PCT/US99/28551 PCT/US99/30095 PCT/US99/30999 PCT/US00/00376 PCT/US00/03565 PCT/US00/13705 PCT/US99/20594 PCT/US00/04341 PCT/US00/04342 PCT/US00/05841 PCT/US00/06884 PCT/US00/08439 PCT/US00/14042 PCT/US00/14941 PCT/US00/15264 PCT/US00/22031 CT/US00/23522 PCT/US00/30873 NUMBER: 09/872035 NUMBER: 09/924419 2001-08-06 NUMBER: 09/927796 2001-08-06 09/802706 NUMBER: 09/866034 NUMBER: 09/918585 NUMBER: 09/929404 2001-08-13 NUMBER: 09/946374 : 2001-09-04 NUMBER: 09/882636 09/941992 -06-1 FILING DATE: 2000-08 APPLICATION NUMBER: FILING DATE: 2000-11 LING DATE:

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Pred. No. 17;
6; Mismatches 19; Indels 13;
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                         PCT/US01/06520
                                                                                             NUMBER: PCT/US01/17800
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PLICATION NUMBER: PCT/US00/32678
                                                                                                                                          NUMBER: PCT/US01/21066: 2001-06-29
                                                PCT/US01/06666
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-08-29
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Best Local Similarity 33.3%;
Matches 19; Conservative
                                               ICATION NUMBER: PCT
NG DATE: 2001-03-01
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US-10-001-054-42
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PLICATION NUMBER: 60/078910
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ING DATE: 1998-02-27
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APPLICATION NUMBER: 60/074092
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1: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
1: ACIDS ENCODING THE SAME
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Best Local Similarity 33.3%; Pred. No. 17;
Matches 19; Conservative 6; Mismatches 19; Indels 13; Gaps
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13.7%; Score 61.5; DE
Best Local Similarity 33.3%; Pred. No. 17;
Matches 19; Conservative 6; Mismatches
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CURRENT APPLICATION NUMBER: US/10/121,049
CURRENT FILING DATE: 2002-04-12
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US20030022239A1
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090538
FILING DATE: 1998-06-24
                                                                                                                                                                                         NUMBER: 60/091360
1998-07-01
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
60/090349
                                      60/090429
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NUMBER: 60, --
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; ORGANISM: Homo Sapien
US-10-121-049-132
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RESULT 10 US-10-123-904-132

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19; Indels 13; Gaps
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Pred. No. 17;
6; Mismatches 19; Indels 13
                                                                                     DB 9; Length 333;
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CURRENT FILING DATE: 2002-06-19
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                                                                                     Ouery Match 13.7%;
Best Local Similarity 33.3%;
Matches 19; Conservative.
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Best Local Similarity 33.3%;
Matches 19; Conservative
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NUMBER OF SEQ ID NOS: 550
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; ORGANISM: Homo Sapien
US-10-175-746-132
; TYPE: PRT; ORGANISM: Homo Sapien
US-10-140-470-132
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Best Local Similarity 33.3
Matches 19, Conservative
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US-10-123-904-132
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Smith, Victoria

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
13.7%; Score 61.5; DB 9; Length 33
Best Local Similarity 33.3%; Pred. No. 17;
Matches 19; Conservative 6; Mismatches 19; Indels
                                                                                                                                                                                                                            - See File Wrapper or Palm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - See File Wrapper or Palm
                                                                                                                                                                             US/10/176,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/176,921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 AVCGOPGMPRDPWDLPVGORRTLERHIL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/10176921
US20030027276A1
Timothy A.
                                            Watanabe, Colin K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior Application removed NUMBER OF SEQ ID NOS: 550
                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo Sapien
US-10-176-918-132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Homo Sapien US-10-176-921-132
                                                                                                                                                                          CURRENT APPLIC
                                                                                                                                                                                                                                            NUMBER OF SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT B
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INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC INVENTION: ACIDS ENCODING THE SAME 72 AVCGQPGMPRDPWDLPVGQRRTLLRHIL-----VSDRYRFLYCYVPKVACSNWK 120 18 AICSQ-GAASQP-DLDLASRRLLORALAAALPHRSGVSERWRTFY---PNCPCLRWR 69 DB 9; Length 333; 19; Indels See Palm or File Wrapper Ouery Match 13.7%; Score 61.5; C Best Local Similarity 33.3%; Pred. No. 17; Matches 19; Conservative 6; Mismatches US/10/137,865 completed: March 21, 2003, 11:56:29 he: 17.6094 secs ; TYPE: PRT ; ORGANISM: Homo Sapien US-10-137-865-132

RESULT 15

οy g APPLICATION NUMBER: US/07/908,245 FILING DATE: 19920702 31,284 REFERENCE/DOCKET NUMBER: E CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: 1205 amino acids N-termina TISSUE TYPE: Aorta CELL TYPE: Endothelial NAME: Pabst, Patrea L. REGISTRATION NUMBER: 404-815-6555 INFORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTICS single protein Bovine AMINO ACID linear FILING DATE: 1 CLASSIFICATION: SOURCE: 8 STRANDEDNESS: MOLECULE TYPE: ANTI-SENSE: N FRAGMENT TYPE: HYPOTHETICAL:

> Sequence Sequence S Sequence Sequence Sequence

62 59

Sequence Sequence NAME/KEY: Binding-site

us-09-727-739b-17.rai

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NAME/KEY: Domain
LOCATION: 1085.1086
OTHER INFORMATION: /note= "Potential proline directed
OTHER INFORMATION: phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Domain
LOCATION: 1022.1203
OTHER INFORMATION: /note= "Potential proline directed
OTHER INFORMATION: phosphorylation site"
                                                                                                                                                                                                                                                                                                  /note= "Potential proline directed phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                        /note= "Potential proline directed phosphorylation site"
                       /note= "Potential proline directed
phosphorylation site"
                                                                                                                /note= "Potential proline directed phosphorylation site"
                                                                                                                                                                                                       /note- "Potential proline directed phosphorylation site"
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phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Domain
LOCATION: 168.170
OTHER INFORMATION: /note- "CAMP dependent
OTHER INFORMATION: phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "cAMP dependent
phosphorylation site"
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phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Domain
LOCATION: 141..143
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Domain
LOCATION: 872.873
OTHER INFORMATION: ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATION: 114..116
HER INFORMATION:
HER INFORMATION:
    LOCATION: 602.603
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 869..870
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                      NAME/KEY: Domain
LOCATION: 838.839
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                             LOCATION: 727..728
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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phosphorylation site"
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phosphorylation site"
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phosphorylation site"
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                                                                                                                                                              /note= "FAD-Pyrophosphate binding domain"
LOCATION: 496..512
OTHER INFORMATION: /note= "CA++/CAM binding domain"
                                                                                                                                                                                                                                                        /note- "FAD-Isolalloxanthine binding domain"
                                                                                                                                                                                                                                                                                                                 KEY: Binding-site
108: 1012-1.1030
INFORMATION: ^/note= "NADPH-Ribose binding INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "NADPH-Ribose binding domain"
                                                                                             "FMN binding domain'
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                                                                           LOCATION: 651.678
OTHER INFORMATION: /note=
                                                                                                                                                                                                                      ME/KEY: Binding-site
CATION: 937..947
HER INFORMATION: /note
HER INFORMATION: bindi
                                                                                                                                 Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Binding-site
LOCATION: 1111, 1124
OTHER INFORMATION: /not
OTHER INFORMATION: doma
                                                        Binding-site
                                                                                                                                                   LOCATION: 795..806

OTHER INFORMATION:

OTHER INFORMATION:
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LOCATION: 459.460
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 282..283
OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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R INFORMATION:
R INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 738.740

OTHER INFORMATION: /note- "CAMP dependent
COTHER INFORMATION: phosphorylation site"
US-07-908-245-2 NAME/KEY: Domain
COATION: 1051.1053
OTHER INFORMATION: phosphorylation site" /note= "cAMP dependent phosphorylation site"

Indels 20; Gaps Score 67; DB 1; Length 1205; Pred. No. 7; 4; Mismatches 25; Indels 2 Query Match
Best Local Similarity 35.5%;
Matches 27; Conservative

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GODECKE, Axel
ENTION: DAM EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
ENTION: TREATMENT OF VASCULAR DISORDERS
                        INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                        8 CALALLGLALAIC-SQGAAS----QPDLDLASRRLLQRALAAALPHRSGVSERWRTFYPNC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SRAPAPATPHAPDHSPA----PNS 58
                                                                                                                                                                                                                                                                                                                                                                         20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 CALALLGLALAIC-SQGAAS---QPDLDLASRRLLQRALAAALPHRSGVSERWRTFYPNC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 67; DB 4; Length 1205;
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                                                                                                                                                                                                                                                                                                                                                                         Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION: TREATMENT
TITLE OF INVENTION: TREATMENT
FILE REFERENCE: 511169-2004
CURRENT APPLICATION NUMBER: U
CURRENT FILING DATE: 1998-07
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 35.5
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 35.5
Matches 27; Conservative
                                                                                                                                                                                                                                                                    ; TYPE: PRT; ORGANISM: Cytomegalovirus US-09-123-708-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 PILTRPPEGPKFPRVK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 PCLRWRPRKVKGPQLK 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Bos taurus
US-09-123-624-6
                                                                                                                                                                                              NUMBER OF SEQ ID NC
SOFTWARE: Patentin
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID
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CALALLGLALAIC-SQGAAS---QPDLDLASRRLLQRALAAALPHRSGVSERWRTFYPNC 63
                                   --SRAPAPATPHAPDHSPA----PNS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 CALALLGLALAIC-SQGAAS---QPDLDLASRRLLQRALAAALPHRSGVSERWRTFYPNC 63
                                                                                                                                                                                                                                                 : Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patentin Release #1
                            15 CGLG-LGLGLCGKQGPASPAPEP
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                                                                    64 PCLRWRPRKVKGPQLK 79
                                                                                                     59 PTLTRPPEGPKFPRVK 74
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                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 27; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                      TY: Lexington
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1100 CVEGCECDPGFVLSGLQCVSRSECGCLDSTAGXVKVGERW--FKPGCRQLCICEGNNRTR 1157
                                                                                                                                                                                                                                                                                                                      20 CSQGAASQPDLDLASRRLLQRALAAALPHRSG---VSERWRTFYPNC------P 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IYDROPHOBICALLY-MODIFIED PROTEIN COMPOSITIONS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 15;
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                                                                                                                                                                                                                                                                       Pred. No. 1.6e+02;
7; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58.5, E
Pred. No. 21;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CALALLGLALAICSQGAASQPDLDLASRRLL---
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Best Local Similarity 26.2%;
Matches 17; Conservative
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Best Local Similarity 30.0%;
Matches 21; Conservative
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                                                                                    NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-325-256-24
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                                                                                                                                                                                                                                                                                                                                                                                                                   |: ||
| Db | 1158 CVLWR || 1162
                                                                                                                                                                                           ; MOLECULE TYPE:
US-08-276-967-2
                                                                                                                                                                                                                                                                                                                                                                                            65 CLRWR 69 .
                                                                                                                                                          STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PE
SEQ ID NO 24
LENGTH: 396
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PERLICANT: Garbers, David L.
RITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
FITLE OF INVENTION: Sperm
                                                                   THE SCRIPPS RESEARCH INSTITUTE 10666 No. 6074872th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 CALALLGLALAICS-QGAASQPDLDLASRRLLQRALAAA 45
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                                                                                                                                                                                                                                                               RRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/648,322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08276967 Patent No. 5851817
                                                                                                                                                                                                                                                                                                                                                         NAME: Fitting, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 13.9%;
Local Similarity 48.7%;
les 19; Conservative
                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
FRAGMENT TYPE: C-terminal
US-08-648-322-3
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                    CITY: La Jolla
STATE: California
                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE
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                                                                   ADDRESSEE:
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                                                                                                                                       COUNTRY:
                                                                                  STREET:
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Best Local S
Matches 19
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65 VELVSWKPLLQAIART-----VQYKLKTLYPNIPTTDYDPLQVEEPFLLVK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                     30 LDLASRRLLQRALAAALPHRSGVSERWRTFYPNCPCLRWRPRKVKGPQLKAK 81
                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 479;
                                                                                                                                                                                                                                                                                                                                                                                              20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN OF REPLICATION COMPLEX GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT Embarcadero Center, Suite 3400 ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                        12.7%; Score 57; 30.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/484,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08484106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 30.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DATA
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION
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                                                                                      PELECOMMUNICATION
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US-08-484-106-10
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11 CCLALLALPAQSCGPGRGPVGRRRYARKQLVPLLYKQFVPGVPERTLGASGPAEGRVARG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
12.9%; Score 58; DB 4; Length 802;
Best Local Similarity 30.0%; Pred. No. 58;
Matches 24; Conservative 5; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LALLGLALAICSQGAASQPDLDLASRRL-----LQRALAAALPHRSGVSE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN OF REPLICATION COMPLEX GENES
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                                                                                                                                                                                                                                                                                                          MAMMALIAN ADHESION PROTEASE PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                             StSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 99-39
CURRENT APPLICATION NUMBER: US/09/632,098
CURRENT FILING DATE: 2000-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DATA:
R: US/08/484,105
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Baindur, Nand
Sishop, Paul D.
NTION: MAMMALTEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
US-09-632-098-2
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                                        53 SERWRTFYPN 62
                                                                               71 SERFRDLVPN 80
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                                                                                                                                              RESULT 8
US-09-632-098-2
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US/08/469,260A

NUMBER:

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PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER: US/08/424,550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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    : 100 ABBOTT PARK ROAD ABBOTT PARK
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                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity
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STREET: 0.
Boston
                                                               USA
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US-08-469-260A-344
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    STREET:
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                                                                                                    Gaps
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                                                                                                                                                     65 VELVSWKPLLQAIART-----VQYKLKTLYPNIPTTDYDPLQVEEPFLLVK 110
                                                                                                                               30 LDLASRRLLQRALAAALPHRSGVSERWRTFYPNCPCLRWRPRKVKGPQLKAK 81
                                                                                                Indels
                                                           DB 1; Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 12.7%; Score 57; DB 4; Length 834; Best Local Similarity 25.7%; Pred. No. 8; Matches 28; Conservative 12; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             550 SPOVLGVRIQNGRHPLMELCARTFVPNSTECGGDKGRVKVITGPNSSGK 598
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                                                                                                                                                                                                                                                                                                                                                      PPLICANT: ACHARYA, Samir
ITLE OF INVERTION: COMPOSITIONS, KITS, AND METHODS FOR E.
ITLE OF INVENTION: NUCLEOTIDE MODULATION OF DNA MISMATCH
ITLE OF INVENTION: PROTEINS
                                                                                                20;
                                                                        ); Pred. No. 41;
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER: US/09/143,571
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                                                                                                                                                                                                                                                            Sequence 29, Application US/09143571
Patent No. 6333153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -80-86
                                                                      1 Similarity 30.89
                                                                                                                                                                                                                                                                                                                     SHEL, Richard
ADIA, Scott
// MOLECULE TYPE: protein US-08-484-106-10
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; ORGANISM: Homo sapiens
US-09-143-571-29
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                                                                                            Matches
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Gaps

DB 4; . Length 47;

protein

4BER: US/08/176,427B 30-DEC-1993

Vertebrate Em Proteins and

Clifford

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11 CCLALLALSAQSCGPGRGPVGRRRYVRKQLVPLLYKQFVPSMPERTLGASGPAEGRVTRG 70
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                                                                                                                                                                                                                                                                         Vertebrate Embryonic Pattern-Inducing
Proteins and Uses Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28; Indels
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                                                                                                                                                                                                                                                                                                                                   HOAG & ELIOT LLP
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-JUNE-1995
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                                                                                                                                          Application US/08460900C 6165747
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Best Local Similarity 28.6
Matches 20; Conservative
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ADDRESSEE: FOLEY, H
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATION NUMBER
                                               53 SERWRTFYPN 62
                                                                           71 SERFRDLVPN 80
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US-08-460-900C-9
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                                                                                                                                                                                28; Indels 15;
                                                                                                                                                  DB 1; Length 396;
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                                                                                                                                                                                7; Mismatches
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                                                                                                                                                                                                            8 CALALLGLALAICSQGAASQPDLDLASRRLL--
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                                                                                                                                                                                                                                                                                                                                                                               Application US/08356060A
(617) 227-7400
                                                                                                                                                 Ouery Match 12.6%;
Best Local Similarity 28.6%;
Matches 20; Conservative
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Best Local Similarity 28.6%;
Matches 20; Conservative
               TELEFAX: (617) 227-5941 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RE: ASCII(text)
APPLICATION DATA
                                               CHARACTERISTICS
                                                                                                     MOLECULE TYPE: protein
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TITLE OF INVENTION:
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71 SERFRDLVPN 80
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TELEPHONE:
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08-356-060A-9
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Search completed: March 21, 2003, 11:42:33 Job time: 20.2403 secs

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Scoring table:

Searched:

Minimum DB Maximum DB

Database

score:

Title:

Sequence:

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Run on:

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Human Secreted pro
Human DiTHP polype
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Human secreted pro
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Human Nerv protein
Novel human diagno
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Human PRO4400 poly
Human PRO4400 prot
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Peptide #10620 enc
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Human polypeptide,
Human drug metabol
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Novel human diagno
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                                                                                                                          ropionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine MSH5 (mMSH)
Propionibacterium
Human ORFX proteir
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anticonvulsant.
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Protein #8062
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26.111
/note= "Mature PPSS-II''"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "PPSS-II'' pro-sequence"
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1..25
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/note=
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Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU07668
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Novel human diagno
Angiotensin conver
Sequence of prepro
Propionibacterium
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Rainbow trout prep
Rainbow trout prep
                                                                                                                                         March 21, 2003, 11:35:23 ; Search time 53.1502 Seconds
   (without alignments)
   215.607 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a cocre greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                        .....RWRPRKVKGPQLKAKEDLER 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1994_DAT
/SIDS1/gcgdata/geneseq-geneseqp-emb1/AA1995_DAT
/SIDS1/gcgdata/geneseqp-emb1/AA1997_DAT
/SIDS1/gcgdata/geneseqp-emb1/AA1997_DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                       908470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'geneseq/geneseqp-emb1/AA1980.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XSIDSI) goddata/geneseg/genesegp-embl/AA198
SIDSI) goddata/geneseg/genesegp-embl/AA198
SIDSI) goddata/geneseg/genesegp-embl/AA198
SIDSI) goddata/geneseg/genesegp-embl/AA198
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SIDSI) goddata/geneseg/genesegp-embl/AA198
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                   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS1/gcgdata/geneseq/geneseqp-embl/
/SIDS1/gcgdata/geneseq/geneseqp-embl
                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                             908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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AAU30069
ABB42770
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450
1 MRVSQIHCALALLGLALAIC....
                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 200000000
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Match 1
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78.6
19.0
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"Prosomatostatin II'

87..111 /note= "1 96..97

Cleavage-site

Novel human secret Peptide #10276 enc

85.5 79.5 70.5 69 67

Result

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Pept 1de

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The invention relates to an Oncorhynchus mykiss somatostatin polypeptide containing a portion of preprosomatostatin I (PPSS-I) and/or a portion of preprosomatostatin I (PPSS-II). The protein sequences and their associated polynucleotides are useful for identifying modified associated polynucleotides are useful for identifying modified somatostatin polypeptide which functions as somatostatin agonist useful cor research, therapeutics or diagnostics, including medical and veterinary applications. The wild-type somatostatin and its modified the pitultary (e.g. acromagaly) or gastroenteropancratic tissues (e.g. gastrinoma, glucagonoma, carcinoid syndrome), to cause tumours hinthy their effects on cell prolliferation and apoptosis and as adjuncts in the treatment of diabetes mellitus via inhibition of growth hormone and glucagon. In addition, dysfunctional somatostatin secretion is associated with acquired immunodeficiency syndrome (AIDS) and various neurological disorders (e.g. epilepsy, Alzheimer's disease and treatment of such conditions. Nucleic acids encoding the polypeptides are
   Rainbow trout; somatostatin; preprosomatostatin; hypersecretion; PPSS-I; PPSS-II'; endocrine tumour; pituitary gland; glucagonoma; AIDS; gastroenteropancreatic tissue; acromegaly; gastrinoma; diabetes mellitus; carcinoid syndrome; call proliferation; apoptosis; growth hormone; glucagon; acquired immunodeficiency syndrome; neurological disorder; HIV; eppleagon; acquired immunodeficiency syndrome; neurological disorder; HIV; neoplasm; metastasis; gene therapy; antidiabetic; nootropic; cytostatic; anti-human immunodeficiency virus; osteopathic; anticonvulsant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of such conditions. Nucleic acids encoding the polypeptides are gene therapy and fusion peptides can be targeted to neoplasms metastases, inhibiting the release of their secretory products. once represents 0. Whylas PBS-II' protein. features for this sequence are specifically claimed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New somatostatin polypeptides derived from Oncorhynchus mykiss, u for treating diabetes mellitus, acromegaly, gastrinoma, acquired immunodeficiency syndrome and neurological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .101
.te= "PPSS-II' pro-sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "PPSS-II' pre-sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .115
te- "Prosomatostatin II'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Mature PPSS-II'"
74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Encoded by CAA"
                                                                                                                                                                                                                                                                                                                                                                                                /note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kittelson JD;
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 3; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2000; 2000CA-2325169
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100..101
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Note: The features for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NDSU-) NDSU RES FOUND.
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102..11
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note-
                                                                                                                                                                                                                                                                         Oncorhynchus mykiss:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS12934.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-2001.
                                                                                                                                                                                                                                                                                                                                    Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an Oncorhynchus mykiss somatostatin polypeptide containing a portion of preprosomatostatin I (PPSS-I) and/or a portion of preprosomatostatin I (PPSS-I) and/or a portion of preprosomatostatin I (PPSS-I) and or a portion of preprosomatostatin I (PPSS-II). The protein sequences and their associated polynucleotides are useful for identifying modified of contact the polypeptide which functions as a somatostatin agonist useful for research, therepeutics or diagnostics, including medical and version are useful for the wild-type somatostatin and its modified version are useful for treating hypersecretion from endocrine tumours in attributery (e.g. acromegaly) or gastroenteropanceatic tisques (e.g. through their effects on cell proliferation and apoptosis and as adjuncts in the treatment of diabetes mellitus via inhibition of growth hormone and glucagon. In addition, dysfunctional somatostatin secretion is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and glucagon. In addition, dysfunctional somatostatin secretion is associated with acquired immunodeficiency syndrome (AIDS) and various neurological disorders (e.g. epilepsy, Alzhehmer's disease and Huntington's disease) and somatostatin antagonists are effective in the treatment of such condutions. Nucleic acids encoding the polypeptides are useful in gene therapy and fusion peptides can be targeted to neoplasms and their metastases, inhibiting the release of their secretory products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and uneir metastases, inhibiting the release of their secretory proditions are sequence represents 0. Mykiss ppsS-II'' protein.

Note: The features for this sequence are specifically claimed in the specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New somatostatin polypeptides derived from Oncorhynchus mykiss, u
for treating diabetes mellitus, acromegaly, gastrinoma, acquired
immunodeficiency syndrome and neurological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rainbow trout preprosomatostatin II (PPSS-II') polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 100.0%; Score 450; DB 22;
Local Similarity 100.0%; Pred. No. 3.2e-49;
hes 86; Conservative 0; Mismatches 0;
/note= "Dibasic cleavage site" 98..111
/note= "SS-14 variant peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                        Kittelson JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU07667 standard; Protein; 115 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 3; 52pp; English.
                                                                                                                                                                                                                                  01-DEC-2000; 2000CA-2325169.
                                                                                                                                                                                                                                                                                                 99US-0168934.
                                                                                                                                                                                                                                                                                                                                                                                                                        Moore CA,
                                                                                                                                                                                                                                                                                                                                                             (NDSU-) NDSU RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-425997/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS12935.
                                                                                                                   CA2325169-A1
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                               Peptide
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The invention relates to an Oncorhynchus mykiss somatostatin polypeptide containing a portion of preprosomatostatin I (PPSS-II) and/or a portion of preprosomatostatin II (PPSS-II); The protein sequences and their associated polynuclectides are useful for identifying modified somatostatin polypeptide which functions as a somatostatin agonist useful for research, therapeutics or diagnostics, including medical and version are useful for treating hypersecretion from endocrine tumours in the pituitary (e.g. acromegaly) or gastroenteropanceatic tissues (e.g. through their effects on cell proliferation and apoptosis and as adjuncts and glucagonoma, carcinoid syndrome), to cause tumour shrinkage through their effects on cell proliferation and apoptosis and as adjuncts and glucagon. In addition, dysfunctional somatostatin secretion is associated with acquired immunodeficiency syndrome (AIDS) and various neurological disorders (e.g. epilepsy, Alzheimer's disease and managonists are effective in the treatment of such conditions. Nucleic acids encoding the polypeptides are and their metastases, inhibiting the release of their secretory products. This sequence is managonists are effective their secretory products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ence represents O. Mykiss PPSS-I protein.
features for this sequence are specifically claimed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.0%; Score 85.5; DB 22; Length 114;
Best Local Similarity 52.3%; Pred. No. 0.065;
Matches 23; Conservative 5; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRVSQIHCALALLGLALAICSQGAASQPDLDLASRRLLQRALAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; SEQ ID 7855; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein, SEQ ID NO: 7855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG03774 standard; Protein; 116 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     his sequence represents
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N-PSDB; AAC03780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence , 114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification
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                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPSS-II', PPSS-II'; endocrine tumour; pituitary gland; glucagonoma; AIDS; gastroenteropencreatc tissue; acromegaly; gastroinoma; diabetes mellitus; carcinol syndrome; call proliferation; apoptosis; growth hormone; glucagon; acquired immunodefictency syndrome; neurological disorder: HIV; epilepsy; Alzheimer's disease; Huntington's disease; neuroprotective; neoplasm; metastasis; gene therapy; antidiabetic; nootropic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trout; somatostatin; preprosomatostatin; hypersecretion; PPSS-I;
                                                                                                                                                                   3; Gaps
                                                                                                                                          1 MRVSQIHCALALIGLALAICSQGAASQPDLDLASRRLLQRALAAALPHRSGVSERWRTFY 60
                                                      Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-human immunodeficiency virus; osteopathic; anticonvulsant
                                                                                            6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rainbow trout preprosomatostatin I (PPSS-I) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for treating diabetes mellitus, acromegaly, gastrino 
immunodeficiency syndrome and neurological disorders
                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /nortem "Dibasic cleavage site"
                                                78.6%; Score 353.5; DB
llarity 86.9%; Pred. No. 6e-37;
Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "PPSS-I pre-sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |..24
/note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .114
+e= "Mature PPSS-I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kittelson JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "SS-14 peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     somatostatin polypeptides derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    AAU07666 standard; Protein; 114 AA.
                                                                                                                                                                                                                                       61 PNCPCLRWRPRKVKGPQLKAKEDL 84
                                                                                                                                                                                                                                                                  61 PNCPCL--RPRKVKCP-AGAKEDL 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 2; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2000; 2000CA-2325169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L
Jnote= "c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sheridan MA, Moore CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NDSU-) NDSU RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..88
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note=
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N-PSDB; AAS12933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncorhynchus mykiss.
                                                Query Match
Best Local Similarity
Matches 73; Conserv
     115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA2325169-A1.
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        Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU07666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rainbow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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Gaps

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us-09-727-739b-17.rag

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quantitating a polypeptide in tissue, as molecular weight markers and as
different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are larved from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene theorepy and crhromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                5 QIHCALALIGLALAI-CSQGAASQPDLDLASRRLLQRALAAALPHRSGVSERWRTFYPNC 63
                                                                                                                                                                                                                                                                                                                                                         Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensi
food supplement; medical imaging; diagnostic; genetic disorder
                                                                                                                                                                                                                                                                                                        Score 79.5; DB 21; Length 116;
Pred. No. 0.038;
3; Mismatches 28; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID No 39283; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human diagnostic protein #8915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG08924 standard; Protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 --LLSEPNOTENDALE-PEDLSO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 PCLRWRPRKVKGPQLKAKEDLER 86
                                                                                                                                                                                                                                                                                                        17.7%;
34.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                           Local Similarity 34.9% nes. 29, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                 116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS73111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000;
23-AUG-2000;
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                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                           Query Match
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ABG08924
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imaging of sites expessing (II). (I) and (II) are useful for treating disorders involving aberant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensizes, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess blodiversity amino acid sequences. ABGO0010-ABG3037, represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the vipo int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; wasoactive intestinal polypeptide receptor 2; arterioscierosis; cancer; mayocadial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nmultiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 HCALALLGLALAICSQGAASQPDLDLASRRLLQRALAAALPH----RSGVSERWRTFYPN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiotensin converting enzyme (ACEV) splice variant protein #76
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                     15.7%; Score 70.5; DB 22;
llarity 31.0%; Pred. No. 0.57;
Conservative 4; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Azar I, Khosravi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU02976 standard; Protein; 517 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 CPCLRWRPRKV-----KGPQLK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 CGCGERAPREYPDPSRSWRGPORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-NOV-2000; 2000WO-IL00766.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 26; Consery
                                                                                                                                                                                                                                                                                                                                                                      124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAS06076
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10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Best Local S
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Claim 4; Fig 76; 519pp; English.

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P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
preprosomatostatin-2, prosomatostatin-2 and somatostatin-2; and DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 W 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 W 59
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU55408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                       of
                                                                                    cyclin-dependent kinase
                                                                                                                        polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLALAICSQGAASQPDLDLASRRLLQRA-----LAAALPHRSGVSERWRTFYPNCPCLR 67
                                                                                                                                                                                                                                                                                                       cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous dise
as asbestosis and vascular pathologies involving an endothelial
abnormality such as deep vein thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The inventors claim preprosomatostatin-1, prosomatostatin-1,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 15.6%; Score 70; DB 22; Length 517; Best Local Similarity 37.8%; Pred. No. 3.7; Matches 28; Conservative 7; Mismatches 21; Indels
                                                                                                              vasoactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Somatostatin; growth hormone; peptide hormone; secretion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of preprosomatostatin-2 encoded on pLaS2.
                                                                                    platelet-derived endothelial cell growth factor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ж.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New somatostatin and precursors - produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
112. 125
/label Somatostatin II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP20029 standard; Protein; 125 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hobart P, Crawford R, Pictet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80US-0181046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||| |:| |
404 FPRPFPSPRLSA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 W-RPRKVKGPQLKA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Fig 3; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1982-18113E/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lophius americanus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAN20034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-1981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-AUG-1980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-AUG-2002
14-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP46669-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP20029;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteomyelitis; stem; ELISA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyeliti: uvatis; endophthamitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes polypeptides and nucleic acids useful for accinating against and diagnosing infections, especially useful for treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 IHCALALLGLALAICSQGAASQ-----PDLDLASRR--LLQRALAAALPHRSGVSER 55
                                              resultant precursor (pro SI) is subsequently cleaved to yield SI bases long. Translation of plas2 predicts the sequence of a 120-25 bases long. Translation of plas2 predicts the sequence of a 125 Ab peptide which surprisingly contains a 14 Ab sequence at its carboxy terminus which differs from SI by only 2 Abs, and is termed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17; Indels 15;
he translation of somatostatin mRNA yields a
S1) containing a signal peptide which may be
teransit into the endoplasmic reticulum, and
                                                                                                                                                                                                                                                                                                                                                                                                 Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes immunogenic protein #16304.
                                                                                                                                                                                                                                                                       (Updated on 16-AUG-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                 Score 69.5; DB 3;
Pred. No. 0.78;
7; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Wang S.
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID No 16603; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU55408 standard; Protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 15.4%; Sco
Best Local Similarity 36.1%; Pro
Matches 22; Conservative 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                     precursor (prepro S1) conta
released during the transit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-APR-2001; 2001WO-US12865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Persing DH, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-616774/71.
N-PSDB; AAS59569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                    .125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2001
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P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s and antagonists) that bind to them. Cells useful for identifying a therapeutic agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s and antibodies to the polypeptides are useful for
the presence of or predisposition to a disease associated
a levels of polypeptide. The polypeptides are also useful d
                                                                                                                              and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes propeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by Note: The sequence data for this patent did not form part of the prin specification, but was obtained in electronic format directly from WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 ALLGLALAICSQG--AASQPDLDLASRRLLQRALAAAL------PHRSGVSERWR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stem cell proliferation; haematopoiesis; nerve tissue regeneration
immune suppression; immune stimulation; anti-inflammatory; leukaem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel human secreted polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----APCRREDTRORIVVWHLPVASHYASWRPRVVR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------WRPRKVK 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.3%; Score 69; DB 2
25.8%; Pred. No. 1.5;
iive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 233; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU30069 standard; Protein; 814 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel human secreted protein #560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identifying agents (agonists and expressing the proteins are usefu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rang Yr, Liu C, Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 25.89 es 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccination;
                                                                                                                                                                                                                                                                                                                                                                                                                   190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 TFYPNCPCLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200179449-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determining t
with altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressing
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU30069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
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used to
                                       the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase steem cell proliferation; to regulate heamatopolesis, and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or simulation, as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ed from human
a single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                               to aberrant expression or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived from human foetal
may be used for predicting
samples derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SQIHCALALLGLALAI-CSQGAA---SQPDLDLASRRLLQRALAAALPHRSGVSERWRTF 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          liver. The present sequence is a peptide encoded by a sing
to acid probe of the invention.

The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \ensuremath{\mathsf{Human}} genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #10276 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 27; SEQ ID NO 35405; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                   Score 69; DB 22; Length 814;
Pred. No. 8.6;
8; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 displaying gene expression in samples derive
The present sequence is a peptide encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a single exon nucleic acid promeasuring human gene expression in a sample derived fro
liver. The single exon nucleic acid probes may be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB42770 standard; Peptide; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hanzel DK, Chen W,
                                                                                                                                                                                                                                                                                                                                      15.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                            Local Similarity 32.4
les 23; Conservative
  treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               696 PSSCPALARHP 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 YPNCPCLRWRP 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                      814 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200157277-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-OCT-2000;
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                                                                                                                                                                                                                                                                                         Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB42770;
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
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Indels

Length 95;

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probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human brain expressed single exon probe encoded protein SEQ ID NO: 35766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                          2 LALLYLSLRVNRLLRGNPAYLNTAGSTLGRSSKPSAHFTA-----ASAAASPRRSSLRA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the hum brain. They can be used to measure gene expression in brain cell sam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LALLGLALAI--------CSQGAASQPDLDLASRRLLQRALAAALPHRSGVSE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                               10 LALLGLALAI------CSQGAASQPDLDLASRRLLQRALAAALPHRSGVSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LALLYLSLRVNRLLRGNPAYLNTAGSTLGRSSKPSAHFTA-----ASAAASPRRSSLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO: 35766; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 95;
                       DB 22;
                                               7%; Pred. ...
11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.0%; Score 67.5; 27.7%; Pred. No. 1;
                     15.0%; Score 67.5; 27.7%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                               AAM63661 standard; Protein; 95 AA.
                                                                                                                                                                                                       RW-----RTFYPNCPCLRWRPRK 72
                                                                                                                                                                                                                                                  SWSSWWDRSWWTRC---AWRPRR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US00667
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2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483446/52.
                                          Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epilepsy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157275-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-2001;
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04-OCT-2000;
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                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           brains
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                                                                                                                                                                                                                                                                                                                    RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n relates to single exon nucleic acid probes for expression in a sample derived from human heart (see the present sequence is a protein encoded by one such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           measuring gene expression, the probes are useful for predicting, agnosing, grading, staging, monitoring and prognosing diseases of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . The probes may be used for predicting, measuring and displaying expression in samples derived from the human heart via microarrays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                            2 LALLYLSERVNRLLRGNPAYLNTAGSTLGRSSKPSAHFTA----ASAAASPRRSSLRA 55
                                                                                                                                                                                                     10 LALLGLALAI -------CSQGAASQPDLDLASRRLLQRALAAALPHRSGVSE 54
                                                                                                                                                          29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosing, grading, staging, monitoring and prognosing disease human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein #8062 encoded by probe for measuring heart cell gene
                                                                                                             Length.95;
                                                                                                                                                          Indels
                                                                                                               DB 22;
                                                                                                                                                       20;
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                                                                                                          15.0%; Score 67.5; Di
27.7%; Pred. No. 1;
1ve. 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel DK, Chen W, Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB26063 standard; Protein; 95 AA
                                                                                                                                                                                                                                                                                          55 RW----RTFYPNCPCLRWRPRK 72
                                                                                                                                                                                                                                                                                                                            56 SWSSWWDRSWWTRC---AWRPRR 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention relates
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2000GB-0024263
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                                                                                                                                  Similarity 27.7
23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                measuring human gene
ABA21535-ABA41305). T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488899/53
                                                                  95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular di
congenital heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200157274-A2.
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04-OCT-2000;
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                                                                                                             Query Match
Best Local Simi
Matches 23;
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                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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RESULT 13
AAM76475
ID AAM76

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ant invention relates to human single exon nucleic acid probes es AA110068-AA128459). The present sequence is a peptide encoded or probe. The SENPs are derived from human HeLa cella. The SENPs ed to produce a single exon microarray, which can be used for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide #10620 encoded by probe for measuring placental gene expression.
                                                     Peptide #7341 encoded by probe for measuring cervical gene expression.
                                                                                                          microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LALLYLSLRVNRLLRGNPAYLNTAGSTLGRSSKPSAHFTA-----ASAAASPRRSSLRA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----CSQGAASQPDLDLASRRLLQRALAAALPHRSGVSE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome-derived single exon nucleic acid probes useful for ting gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; microarray; human; placenta; antenatal diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID No 25733; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 27.7%; Score 67.5; Conservative 11; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAM36583 standard; Protein; 95 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
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        12-OCT-2001 (first entry)
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Best Local Similarity
Matches 23; Conserv
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                                                                                                                                 cervical cancer
                                                                                                                                                                                                                          WO200157278-A2.
                                                                                                                                                                                Homo sapiens.
                                                                                                  Probe; human;
                                                                                                                                                                                                                                                                       09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
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bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LALLYLSLRVNRLLRGNPAYLNTAGSTLGRSSKPSAHFTA-----ASAAASPRRSSLRA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LALLGLALAI-------CSQGAASQPDLDLASRRLLQRALAAALPHRSGVSE 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                       gene expression analysis; probe;
                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed probe encoded protein SEQ ID NO: 36781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          provided from general sequences expressed in the de desert of measure gene expression in bon ble the improved diagnosis and treatment remains and myeloma. The present sequence i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.0%; Score 67.5; DB 22; 27.7%; Pred. No: 1; tive 11; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                leukaemia; lymphoma; myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone marrow. They can be used to measure ger
samples, which may enable the improved diagr
such as lymphoma, leukaemia and myeloma. The
protein encoded by one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                 Human; bone marrow expressed exon; microarray; cancer; leukaemia; lymp
                                                                                                                                                                     AAM76475 standard; Protein; 95 AA.
----RTFYPNCPCLRWRPRK 72
                                    (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 RW-----RTFYPNCPCLRWRPRK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 SWSSWWDRSWWTRC---AWRPRR 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001; 2001WO-US00668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488900/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157276-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                    06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
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                                                                                                                                                                                                                     AAM76475;
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55 RW-
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26-MAY

Indels

Best Loca Matches

g ò q RESULT 14 AAM20907 ID AAM XX AC AAM:

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The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for producting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LALLYLSLRVNRLLRGNPAYLNTAGSTLGRSSKPSAHFTA-----ASAAASPRRSSLRA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
15.0%; Score 67.5; DB 22; Length 95;
Best Local Similarity 27.7%; Pred. No. 1;
Matches 23; Conservative 11; Mismatches 20; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 27; SEQ ID No 36852; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: March 21, 2003, 11:38:00 Job time : 55.1502 secs
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                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                  30-JAN-2001; 2001WO-US00663.
                                                                                                                                                                                                                                                                                                                                  27-SEP-2000; 2000US-0236359
04-OCT-2000; 2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 AA;
                                            WO200157272-A2
Homo sapiens.
                                                                                                  09-AUG-2001.
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OM protein

Run on:

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Sequence 1, Appli
Sequence 6, Appli
Sequence 1079, Ap
Sequence 1198, A
Sequence 1198, A
Sequence 1123, App
Sequence 121, App
Sequence 121, App
Sequence 174, App
Sequence 247, App
Sequence 247, App
Sequence 257, App
Sequence 27, App
Sequence 186, App
Sequence 186, App
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 47, Appl
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TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TITLE OF INVENTION: TRACT
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                               5-242-11982
                                                                                                                                                                                                                                                                                                                                                                             US-09-764-846-247

US-09-68-826-35

US-09-0115-247-135

US-09-768-826-54

US-10-012-542-297

US-10-012-542-146

US-09-738-626-6025
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SOFTWARE: FastsEO for Windows Version 2.0
SUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                               US-10-036
US-10-025
US-10-025
US-09-83
US-09-83
US-10-091
US-10-091
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COHEN, MAURICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Application US/09050516
US20010010904A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: Abbott Laboratories
: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,855
FILING DATE: 31-MAR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRANADOS, EDWARD N.
R. HAYDEN, MARK
R. HOGGES, STEVEN C.
R. KRAS, MICHAEL R.
R. KRATOCHVIL, JON D.
R. ROBERTS-RAPP, LISA
                                                                                                                                                                                                                 ,999<u>,</u>9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM Compatible
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MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46, Appl Sequence 433, App Sequence 4393, App Sequence 156, App Sequence 101, App Sequence 101, App Sequence 101, App Sequence 101, App Sequence 614, App Sequence 20, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 55, Appl Sequence 6537, Ap
                                                                                                                                                                              March 21, 2003, 11:53:33 ; Search time 2.12446 Seconds (without alignments) 276.816 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a cacce greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.
                            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221153 seqs, 53462247 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum.Match 100%
Listing first 45 summaries
                                                                                                                                      protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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58
1 SVDNLPPRERK 11
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                                                                                                                                                                                                                                                                                            Title:
Perfect score:
Sequence:
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Database

Result

us-09-727-739b-18.rapb

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Annomax Sequence Listing Engine vers
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001-01-30
                                                                                                                                                                                                    NUMBER: PCT/US01/00666
: 2001-01-30
                                                                                                                                                                                                                                                                              TON NUMBER: PCT/US01/00664
                                                                                                                                                               TE: 2000-09-27
                                                 ION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBER: US 60/234,687
                                                                                                                                 LICATION NUMBER: GB 2
ING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                        01-01-30
                                                                                                                                                                                                                                                               001-01-30
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . LOCATION: (97)
. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-860-343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                    0; Gaps

    consult PALM or file wrapper

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18;
                                                                                                                                                                                                                                                                                                 DB 10; Length 33;
                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                             Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/764,860
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38;
Pred. No.
NAME: Becker, Cheryl L:
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6065.US.Pl
TREECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                                                                                                     inear
No. US20010010904Ale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           933, Application US/09864761
US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 343, Application US/09764860 Patent No. US20020094953A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65.5%;
                                                                                                                                                                                                                                                                                               Query Match 65.5%;
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                    33 amino acids
                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100
Matches 7; Conservative
                                                                                          847/938-2623
                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                    1 SVDNLPPRERK 11
                                                                                                                                                                                                                                                                                                                                                                                            3 SVDSAPPGQRK 13
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NUMBER OF SEQ ID NO
SOFTWARE: Patentin
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                                                                                                                                                                                                                          TOPOLOGY: 11
MOLECULE TYPE:
US-09-050-516-46
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US-09-864-761-43933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-764-860-343
                                                                                            TELEFAX:
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PCT/US01/00670

PCT/US01/00661

PCT/US01/00662

PCT/US01/00665 PCT/US01/00668

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Gaps
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                                                                          DB 10; Length 84;
                                                                                                        Indels
                                                                          Score 35; DB Pred. No. 23; 3; Mismatches
                                                                                                                                                                                                                                          156, Application US/10062254. US20020138882A1
INFORMATION: EXPRESSED INFORMATION: EXPRESSED INFORMATION: SWISSPROT
                                                                        60.3%;
54.5%;
                                                                        Ouery Match
Best Local Similarity 54.5
Matches 6; Conservative
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INVENTION: Polynucleotides Encoding Proteins Involved In Plant Metaboli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P. INVENTION: STE20-RELATED PROTEIN KINASES ADDITION: 240/300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATION NUMBER: US/09/291,417A
                            ICATION NUMBER: US/10/062,254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ION NUMBER: US 60/081,784
                                                      APPLICATION NUMBER: 09/630,346
FILING DATE: 2000-07-28
                                                                                                                                                          : 1999-09-30
NUMBER: 60/157287
                                                                                     146511
                                                                                                                NUMBER: 60/156006: 1999-09-23
                                                                                                                                                                                                                                                                 NUMBER: 60/172958
: 1999-12-21
                                                                                                                                                 NUMBER: 60/156899
                                                                                                                                                                                                         NUMBER: 60/169767
                                                                                                                                                                                                                                       NUMBER: 60/171054
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US-09-291-417-30
                                                                                                                                                                                                                       -12-09
                                                                                                                                                                                         -10-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.0
Matches 6. Conservative
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Best Local Similarity 100
Matches 6: Conservative
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                                                                                                                              ved In Plant Metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12; Length 214;
                                                                                                                              TION: Polynucleotides Encoding Proteins Invol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                        09/630,346
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Best Local Similarity 60.0
Matches 6, Conservative
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RGANISM: Glycine max
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9 SLDHLPPSEQ 18
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DETECTING DISEASES OF THE GASTROINTESTINAL
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                                                                                                                                                                                                                                                                                                                                                                                                        rricant: Xu, H. Howard
TTLE OF INVENTION: Identification of Essential Genes in
TTLE OF INVENTION: Prokarvotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 1
Pred. No. 2.7e+
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/09/815,242
                                   Application US/09815242
020061569A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 DATE: 2001-03-21
FION NUMBER: 60/191,078
DATE: 2000-03-21
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: 2000-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER: 60/257,931.
: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -10-2
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US-09-815-242-14001
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Best Local Similarity 85.
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742 DSLPPRE 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISEASE-INDUCED POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 9; Le
Pred. No. 1.4e+02;
1; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Full Length Mammalian (Human) PAK5hu
US-09-291-417-103
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ION 0.103
LENGTH: 591
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Application US/09533029 . US20030046723A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
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Best Local Similarity 85.7%;
Matches . 6; Conservative
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APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-REI
                                                                                                                   Heard, Jacqueline
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                   maha, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: G1034
US-09-533-029-104
                                                                                                                                                                                                                                                                                                                                                                                                                                            Guo-Liang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Ver.
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86 NLPPRKR 92
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529 DNLPPR 534
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RESULT 8 US-09-291-417-103

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NUMBER OF SEQ SOFTWARE: Pate

3 DNLPPR 8

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Gaps

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us-09-727-739b-18.rapb

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Score 34; DB 10; Length 299;
Pred. No. 1.4e+02;
                                                                                                                                                                Score 34; DB 10;
Pred. No. 1.4e+02;
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20061569A1
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                                                                                                               ORGANISM: Staphylococcus aureus
US-09-815-242-5614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRGANISM: Escherichia coli US-09-815-242-10205
                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 6; Conservative
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Best Local Similarity 77.6
Matches 7; Conservative
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33 VDNLPP 38
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MOLECULE TYPE: No. US20010010904Ale
U;-09-050-516-47
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020061569A1
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: 100 Abbott Park Road
Abbott Park
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TYPE: amino acid
STRANDEDNESS: single
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Best Local Similarity 60.0
Matches 6; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                            COMPUTER READABLE FORM
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TELEFAX:

us-09-727-739b-18.rapb

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THER INFORMATION: Amino acid sequence encoded by S. aureus coding region cloned CTHER INFORMATION: expression in E. coli. US-09-828-523A-86
                                                                                             The Pharmacia & Upjohn Company
NENTION: ANTIMICROBIAL METHODS AND MATERIALS
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
58.6%; Score 34; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0;
                                                                                                                               FILE REFERENCE: 268.62120101
CURRENT APPLICATION NUMBER: US/09/828,523A
CURRENT FILING DATE: 2001-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: March 21, 2003, 11:56:31 Job time: 4.12446 secs
                                 Application US/09828523A
0020168697A1
                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                      NUMBER OF SEQ ID
SOFTWARE: PatentI
SEQ ID NO 86
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Pred. No. 1.5e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Identification of Essential Genes in
APPLICANT: The Pharmacia & Upjohn Company...
TITLE OF INVENTION: ANTIMICROBIAL METHODS AND MATERIALS
                                                                                                                                                                                                                                                                           Score 34; DB 9;
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Mismatches
                                                     US/09/828,523A
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FastSEQ for Windows Version 4.0
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120061569A1
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US-09-815-242-12527
                                                                                                                                                                                                                    ORGANISM: Staphylococcus aureus
US-09-828-523A-20
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Best Local Similarity 100.0%;
Matches 6; Conservative C
                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 20
LENGTH: 303
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Best Local Similarity 100.
Matches 6; Conservative
                                                                                    PRIOR APPLICATION NUMBER
PRIOR FILING DATE: 2000-
                                                                                                                             NUMBER OF SEQ ID NOS
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39 VDNLPP 44
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SEQ ID NO 12527
LENGTH: 303
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PRIOR FILI
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39 VDNLPP 44

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Length 311;

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                    Sequence 4, A Sequence 5, A Sequence 5, A Sequence 2, A Sequence 5, A Sequence 5, A Sequence 2, A Sequence 3, Sequence 2, A Sequence 2, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 1, A Sequence 44, A Sequenc
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APPLICANT: MCGNIGLE, BRIAN
APPLICANT: MCSNEEL DANIEL
TITLE OF INVENTION: SOYBEN GLUTATHIONE-S-TRANSFERASE ENZYMES
TITLE OF INVENTION: SOYBEN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REPRENCE: C1-1108-A
CURRENT APPLICATION NUMBER: US/09/24/373B
CURRENT FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 56
SOFTWARE: MICTOSOFT OFFICE 97
SEQ ID NO 52
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APPLICANT: O'KEEFE, DANIEL
TITLE OF INVENTION: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFREENCE: CL-1108-A
CURRENT APPLICATION NUMBER: US/09/247,373B
CURRENT FILING DATE: 1999-02-10
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Pred. No. 9.8;
2; Mismatches 0; Indels
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1997-09-05
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US-08-3
US-08-9
US-08-9
US-08-5
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US-09-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 67.2%;
Best Local Similarity 75.0%;
Matches 6; Conservative
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PRIOR FILING DATE: 1997-0
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) ORGANISM: SOYBEAN
US-09-247-373B-52
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; ORGANISM: SOYBEAN
US-09-247-3738-34
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US-09-247-373B-34
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LENGTH: 219
TYPE: PRT
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LENGTH: 224
  SOFTWARE:
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Sequence 5085, Appl
Sequence 5085, Appl
Sequence 317, Ap
Sequence 2, Appli
Sequence 2, Appli
Patent No. 5169835
Patent No. 5169835
                                                                                                                                          March 21, 2003, 11:41:02; Search time 2.07725 Seconds (without alignments) 155.808 Million cell updates/sec
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Sequence 12,
Sequence 12,
Sequence 48,
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Sequence 3
Sequence 5
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/cgn2_6/ptodata/2/laa/5A_COMB.pep:*
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/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                  GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-247-373B-34
US-09-134-001C-5085
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                                                                                                             protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                           US-09-727-739B-18
58
1 SVDNLPPRERK 11
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Pred. No.
                                                                                                                                                                                                                        Score 36;
Pred. No.
                                                                                                                                                             ORGANISM: Staphylococcus epidermidis US-09-134-001C-3917
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09125028A Patent No. 6190707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2, Application US/08894344C
. 6172196
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APPLICANT: COLAVIZZA, Didier
APPLICANT: LOIEZ, Annie
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kozo
                                                               PRIOR FILING DATE: 1997-01
NUMBER OF SEQ ID NOS: 567-
SEQ ID NO 3917
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257 IDVLPPKER 265
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CURRENT APPLICATION NUMBER: US/09/134,001C
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                                                                                                                                                                                                                                                                            APPLICANT: Lyun Dougette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATIN
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAREDITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PREGNANCY SPECIFIC PROTEINS APPLICATIONS
    Score 39; DB 4; Length 224; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 248;
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                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             917, Application US/09134001C
6380370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5085
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Query Match
Best Local Similarity 75.0
Matches 6; Conservative
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CURRENT APPLICATION DATA:
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Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                    3 DNLPPRER 10
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LENGTH: 424
.69835-6
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PRIOR FILING
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Patent No.
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5169835-6
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TITLE OF INVENTION: DNA ENCODING PROTEIN COMPLEMENTING
TITLE OF INVENTION: YEAGY
TITLE OF INVENTION: LOW TEMPERATURE-SENSITIVE FERMENTABILLITY
TITLE OF INVENTION: NOVEL COLD-SENSITIVE BREAD-MAKING YEASTS FILE REFERENCE: levure sensible froid
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TITLE OF INVENTION: A No. 6087170el VZV Gene, Mutant VZV and Immunogenic TITLE OF INVENTION: A No. 6087170el VZV Gene, Mutant VZV and Immunogenic TITLE OF INVENTION: Compositions NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: COOlev Court of ADDRESSEE: COURT of ADDRESSEE: COOLev Court of ADDRESSE
                                                                                               Gaps
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                                  Score 35; DB 6; Length 419;
Pred. No. 1e+02;
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alo Alto Square
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1185 Avenue of the Americas
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Threonine Kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White, John P. RATION NUMBER: 28,678
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amino acid
Ouery Match
Best Local Similarity 54.5
امات و (Conservative
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                                                                                                                                                                                     245 TINNLNPRENK 255
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TITLE OF INVENTION:
TITLE OF INVENTION:
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 529 DNLPPR 534
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                    Diskette - 3.50 inch, 1440 Kb storage
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                                            COMPUTER: IBM PS/V
OPERATING SYSTEM: MS-DOS Ver3.30
SOFTWARE: PATEMT AID Ver1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,344C
FTLING DATE: IS-AUGUST-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae X2180-18
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LING DATE: 07-AUG-1989
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LLING DATE: 07-AUG-1989
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CURRENT APPLICATION DATA:
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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APPLICANT: WAI-YEE, CHAN
TITLE OF INVENTION: PREGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO
SEQUENCE CHARACTERISTICS
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257 IDVLPPKER 265
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APPLICANT: WAI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-894-344C-2
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PPLICANT: Lynn Doucette-Stamm et al ITLE OF INVENTION: UCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC ITLE OF INVENTION: UUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                  0; Gaps
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NITON: SOYBEAN GLUTATHIONE-S-TRANSFERASE ENZYMES
FE: CL-1108-A
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80;
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                                                                                                                                        Score 34; DB 5; Length 223;
Pred. No. 78;
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58.6%; Score 34; DB 4; Lc
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0;
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Pred. No. 80;
3; Mismatches
                                                                                                                                                                                  Mismatches
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5632
                                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/09247373B Patent No. 6168954
GENERAL INFORMATION:
                                                                                                                                        Match 58.6%; Soc
Local Similarity 100.0%; P:
les 6; Conservative 0;
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DATE: 1997-08-14
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PRIOR FILING DATE: 1997-0
                                                                                 Protein
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NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5632
LENGTH: 305
                                                                 unknown
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Best Local Similarity
Matches 5; Conserv
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FILE REFERENCE: CL-
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200 DSLPPRDK 207
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ORGANISM: SOYBEAN
US-09-247-373B-48
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                                                            ; TOPOLOGY: un;
; MOLECULE TYPE:
PCT-US95-04971-12
                                                                                                                                                                                                                                            6 PPRERK 11
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                                                                                                                                                                                                                                                                                                                       RESULT 13
US-09-247-373B-48
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LENGTH: 229
                                                                                                                                        Query Match
Best Local S
Matches 6
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PEPLICANT: George W. Kemble
FITLE OF INVENTION: A Novel VZV Gene, Mutant VZV and Immunogenic
FITLE OF INVENTION: Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
COOLEY GOALTO GOALTO HUDGLESON & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: PCT/US95/04971
                                                                              PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                  AVIR-004/00US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/235,406
FILING DATE: APRIL 28, 1994
                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/857,534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application PC/TUS9504971 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/235,406
FILING DATE:
                                                                                                                                                                                                                                                          NAME: Luann Cserr
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: AV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5165
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                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                              TELEX: 380816 CooleyPA
INFORMATION FOR SEQ ID NO:
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Best Local Similarity 100.
Matches 6; Conservative
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COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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US-08-857-534-12
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Search completed: March 21, 2003, 11:42:35 Job time : 4.07725 secs

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	GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. OM protein - protein search, using sw model Run on: March 21, 2003, 11:38:15 ; Search time 12.2318 Seconds (Without alignments) (Althout alignments)	1	s, 206047] fying chos	cessing	Database : SPTREMBL_21.* 1: sp_archea.* 2: sp_barchia.* 3: sp_fung1:* 4: sp_human.*		 16: Sp_archeap:* 17: sp_archeap:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution	SUMMARIES Query Score Match Length DB ID	2 120 13 Q90x39 Q90y39 3 114 13 Q90x42 Q90y42 9 114 13 Q90x41 Q90y43 9 115 13 Q90x41 Q90y43 10 116 13 Q90x81 Q90x61 14 13 Q90x81 Q90x61 14 13 Q90x10 Q90x61 14 14 Q90x61 Q90x61 14 14 Q90x61 Q90x61	52 42.6 133 5 095312 52 42.6 133 5 095313 52 42.6 146 5 096313 52 42.6 148 5 096126 52 42.6 148 5 096240 52 42.6 149 5 096311 52 42.6 149 5 096124

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Osteoglossiformes; Osteoglossidae; Osteoglossum.
NCBI_TaxID=109271;
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Matches 14; Conserv
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NCBI_TaxID-7904;
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                                                                                                                              Al-Mahrouki A.A., Irwin D.M., Youson J.H.; "Characterization of variant somatostatin cDNAs from several osteoglossomorphs: molecular identification and comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Al Mahrouki A.A., Irwin D.M., Youson J.H., Characterization of variant somatostatin cDNAs from several osteoglossomorphs: molecular identification and comparative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 114;
                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Actinopterygii, Neopterygii, Teleostei, Osteoglossomorpha,
Osteoglossiformes, Pantodontidae, Pantodon.
                                                                                                                                                                                                                                                                 Score 76; DB 13; Length 11.
Pred. No. 10.0095;
7; Indels
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                                                                                                                                                                                     Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF292651; AAK97068.1; -...
InterPro: IPR004250; Somatostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF292652; AAK97069.1; -
InterPro; IPR004250; Somitostatin. Pfam; PF03002; Somitostatin; 1. SEQUENCE 114 AA: 12494 MW; 454DA57A309CA8F2 CRC64;
                                                                                                                                                                                                                                 Pfam; PF03002; Somatostatin; 1.
SEQUENCE 114 AA; 12352 MW; 7E3D44CB6A27B12F CRC64;
(TrEMBLrel. 20, Last annotation update)
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(TrEMBLrel. 19, Last Sequence update)
(TrEMBLrel. 20, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                            5; Mismatches
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                              Pantodon buchholtzi (Butterflyfish)
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                                                                                                                                                                                                                                                                                62.38;
                                                                                                                                                                                                                                                                                               52.0%;
                                                                                                                                                                                                                                                                                             Local Similarity 52.09
les 13; Conservative
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es 16; Conserv
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                                                                                       NCBI_TaxID-8276;
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01-MAR-2002
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Matches
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Matches
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Eukaryota; Metazoa; Chordata; Cranidata; Vertebrata; Euteleostomi;
Actinopterygii; Chondrostei; Acipenseriformes; Acipenseridae;
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Actinopteryqii; Neopteryqii; Teleostei; Osteoglossomorpha;
Osteoglossiformes; Notopteridae; Chitala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Polygenic expression of somatostatin in the sturgeon Acipenser transmontanus: molecular cloning and distribution of the mRNAs encoding two somatostatin precursors."; J. Comp. Neurol. 0.0-0(2001).
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Al Mahrouki A.A., Irwin D.M., Youson J.H.; Characterization of variant somatostatin cDNAs from several osteoglossomorphs: molecular identification and comparative
                                                                                                                                                                                                                                                                        Score 67; DB 13; Length 115;
Pred. No. 0.02;
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56.0%; Pred. No. 0.15;
1ive 3; Mismatches 8; Indels
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                                                                                                              Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                 Pfam; PF03002; Somatostatin; 1.
enoffence 116 AA; 12616 MW; 72E0C3FF6C80650F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                3; Mismatches
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IPR004250; Somatostatin.
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Boonchuoy C., Boonyawan B., Panyim S., Sonthayanon B.;
"A.CDNA sequence of phosphopyruvate hydratase (enolase) from Black
Tiger Prawn, Penaeus monodon.",
Asia Pac. J. Mol. Biol. Blotechnol. 7:89-94(1999).
-1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE - PHOSPHOENOLPYRUVATE +
                                                                                                                                                                    -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Farrell B.D., Sequeira A.S., O'Meara B.C., Normark B.B., Chung J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jordal B.H.;
"The evolution of agriculture in beetles (Curcullonidae: Scolytinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eŭkaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insec
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Phytophaga; Scolytidae; Hylurgonotus.
NGBL_TAXID=14164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 52; DB 5; Length 132;
Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodom; PD000902; Enolase; 1.
TIGRRAMs; TIGR01060; eno; 1.
PROSITE; PS0104; ENOLASE; 1.
G1yColysis; Lyase; Magnesium; Pyruvate.
SEQUENCE 434 AA; 47265 MM; EB575C6FB541ABD3 CRC64;
                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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Pred. No. 7.4;
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EMBL: A8375337; AAK54795.1; -
Interpro: IPPR000941; Enolase.
Probom: PD000902; Enolase; 1.
                                                                                                                                                                                                                                                                                                                                                          IPR000941; Enolase
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Best Local Similarity 58.8%;
Matches 10; Conservative
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                             EMBL; AF100985; AAC78141.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 64.7%;
nes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 ANAILGVSLAICKAGAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lylurgonotus tuberculatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 ALALIGIALAICSOGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 ALALLGLALAICSQGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 ANAILGVSLAVCKAGAA 36
                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00148; ENOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      PF00113; enolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enolase (Fragment).
                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  096312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
096312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. Farrell B.D., Sequeira A.S., O'Meara B.C., Normark B.B., Chung J.H., Jordal B.H.; "The evolution of agriculture in beetles (Curculionidae: Scolytinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycerate hydro-lyase).

Penaeus monodon (Penoeid shrimp).

Eukaryota, Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Bucarida; Decapoda; Dendrobranchiata; Penaeoidea;

Penaeidae; Penaeus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Betrygota; Neoptera; Bolyphaga; Cucujiformia; Phytophaga; Scolytidae; Aphanarthrum. NCBL_TaxID=113463;
  Al-Mahrouki A.A., Irwin D.M., Youson J.H.;
"Characterization of variant somatostatin cDNAs from several
osteoglossomorphs: molecular identification and comparative
                                                                                                                                                                                                                               y Match
Local Similarity 56.0%; Pred. No. 0.82;
hes 14; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5; Length 216; 2.8;
                                                                                            Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF792653; AAK97070.1; -...
InterPro; IPR004250; Somatostatin.
Prâm; PF03002; Somatostatin; 1.
SEQUENCE 114 AA; 12561 MW; 4E3C32F58E34F971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 216 216
SEQUENCE 216 AA; 22700 MW; 34E3408775FED864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 AA.
Irwin D.M., Youson J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequ
                                                                                                                                                                                                                                                                                                                                                               MRVSQIHCALALLGLALAICSQGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evolution 0:0-0(2001).
EMBL; AF375332; AAK54790.1; -
InterPro; IPR000941; Enolase.
Prodom; PP00113; enolase; 1.
Prodom; PD000902; Enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 ALALLGLALAICSOGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | |:||::||:|
| ATAILGVSLAVCKAGAA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aphanarthrum sp. SCR03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enolase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Platypodinae)
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Matches

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096656

RESULT 8 096656

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Sequeira A.S., Farrell B.D.;
"Evolutionary origins of Gondwanan interactions: How old are Araucaria
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Farrell B.D., Sequeira A.S., O'Meara B.C., Normark B.B., Chung J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             evolution of agriculture in beetles (Curculionidae: Scolytinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Phytophaga; Scolytidae; Pseudohylesinus.
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Persyota; Neoptera; Bidopterygota; Coleoptera; Polyphaga; Cucujiformia; Phytophaga; Scolytidae; Dendroctonus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 5; Length 146;
Pred. No. 3.9;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 146 146
SEQUENCE 146 AA; 15194 MW; 28D98F57787CC168 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15554 MW; 3EF31039835D84A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Pred. No. 4;
4; Mismatches
                                                                                                                      146 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148 AA
                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. J. Linn. Soc. 0:0-0(2001).
EMBL; AY040304; AAK77977.1; -.
InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF375339; AAK54797.1; -
InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD000902; Enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000902; Enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.6%;
                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudohylesinus nebulosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 ANAILGVSLAVCKAGAA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 ALALLGLALAICSOGAA 25
                   20 ANAILGVSLAVCKAGAA 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 58.8 ses 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 58.8
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            beetle herbivores?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enolase (Fragment).
                                                                                                                                                                                                                           Enolase (Fragment)
ENOINI
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM , N. A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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Matches
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096310
                                                                               RESULT 12
096126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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SEQUENCE FROM N.A.
Farrell B.D., Sequeira A.S., O'Meara B.C., Normark B.B., Chung J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEĞUENCE FROM N.A.
Farrell B.D., Sequeira A.S., O'Meara B.C., Normark B.B., Chung J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the evolution of agriculture in beetles (Curculionidae: Scolytinae
                                                                                                                                                                                                                                                                                                                                                                      evolution of agriculture in beetles (Curculionidae: Scolytinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Bergydeta; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Phytophaga; Scolytidae; Xylechinosomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels .
                                                                                                                                                                                                     Eŭkaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inseci
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia: Phytophaga; Scolytidae; Scolytus
NCBL_TaxID=159924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.6%; Score 52; DB 5; Length 146; 58.8%; Pred. No. 3.9; tive 4; Mismatches 3; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 133 AA; 13879 MW; BF8D60C5D97AC008 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 AA; 15404 MW; E3346CF20ADAF658 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                               Created)
Last sequence update)
Last annotation update)
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                                        133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.6%; Score 52; DB 58.8%; Pred. No. 3.6; ive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00113; enolase; 1.
PRINTS; PR01610; CD36ANTIGEN.
ProDom; PD000902; Enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evolution 0:0-0(2001).
EMBL; AF375336; AAK54794.1; -.
InterPro; IPR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                             Evolution 0:0-0(2001).
EMBL, AF375346, AAK44804.1;
InterPro; IPR000941; Enolase.
Pram: PF00113; enolase; 1.
ProDom; PD000902; Enolase; 1.
                                                                          01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xylechinosomus valdivianus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 ALALLGLALAICSQGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ANAILGVSLAVCKAGAA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 42.6'
Best Local Similarity 58.8'
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 ALALLGLALAICSQGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enolase (Fragment).
                                                                                                                                              Enolase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                          Platypodinae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Platypodinae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001
01-DEC-2001
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Q963H3
C963H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             096313;
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Matches
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DB 5; Length 148; 3; Indels ö

Gaps ö

3; Indels

Mismatches

Score 52; DB 5; Length 149; Pred. No. 4;

us-09-727-739b-19.rspt

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Search completed: March 21, 2003, 11:40:48
Job time : 14.2318 secs
Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                   | |:||::||:|
19 ANAILGVSLAVCKAGAA 35
                                                                          9 ALALLGLALAICSOGAA 25
                                                                                                               QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ira A.S., Farrell B.D.;
Lutionary origins of Gondwanan interactions: How old are Araucaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
arrell B.D., Sequeira A.S., O'Meara B.C., Normark B.B., Chung J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   evolution of agriculture in beetles (Curculionidae: Scolytinae
                                                                                                                                                                                                                                                                                                           ukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
terygota, Neoptera, Endopterygota, Coleoptera, Polyphaga,
terygota, Phytophaga, Scolytidae, Hylastes.
CBL_TaxID-141065,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endroctonus terebrans (black turpentine beetle).

ukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

terygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;

toujiformia; Phytophaga; Scolytidae; Dendroctonus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
42.6%; Score 52; DB 5; Length 148;
Best Local Similarity 58.8%; Pred. No. 4;
Matches 10; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 AA; 15404 MW; 633A7D8C7B3D5990 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B09B142A0850D265 CRC64;
                                                                                                                                                                                            01-DEC-2001 (TIEMBLrel. 19, Created)
01-DEC-0001 (TIEMBLRel. 19, Last sequence update)
01-DEC-2002 (TIEMBLRel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              I-DEC-2001 (TrEMBLrel. 19, Created)
I-DEC-2001 (TrEMBLrel. 19, Last sequence update)
I-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                          148 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PR000941; Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          am; PF00113; enolase; 1.
oDom; PD000902; Enolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF375338; AAK54796.1; -
Pro; IPR000941; Enolase.
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                                        20 ANAILGVSLAVCKAGAA 36
                  9 ALALLGLALAICSOGAA 25
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                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         olase (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                               QUENCE FROM N.A.
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SEQUENCE
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human her ramo sapien oryza sativ mus musculu

P04764 P52465 Q05524 P26300 Q9snn0 009043 Q53684 P01166

rattus

P31683 chlamydomon Q12560 aspergillus Q27727 plasmodium

homo sapien homo sapien streptomyce

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MEDLINE-99334921; PubMed-7628684; MEDLINE-99334921; PubMed-7628684; Norce C.A., Kittlison "J.D., Dahl S.K., Sheridan M.A.; Isolation and characterization of a cDMA encoding for preprosomatostatin containing [Tyr7, Gly10]-somatostatin-14 from the endocrine pancreas of rainbow trout, Oncorhynchus mykiss."; Gen. Comp. Endocrinol. 98:253-261(1995).
                                                                                                                                                                                                                                                                                                                                                                              SMS2_ONCMY STANDARD, PRT; 115 AA.

991194,

16-0CT-2001 (Rel. 40, Last sequence update)

16-0CT-2001 (Rel. 40, Last annotation update)

16-0CT-2001 (Rel. 40, Last annotation update)

16-0CT-2001 (Rel. 40, Last annotation update)

Sometostatin 11 precursor [Contains: [Tyr7, G1y2], G1y2], sometostatin 1-14]

Tyr7, G1y10] sometostatin 1-14]

Oncorhynchus mykiss (Raihow trout) (Salmo gairdneri).

Bukaryota: Metazoa: Chordata; Craniata: Vertebrata: Euteleostomi;

Actinopterygli; Neopterygli: Teleostei; Euteleostomi;

Protacanthopterygli; Salmoniformes; Salmonidae: Oncorhynchus.
                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gen. Comp. Endocrinci.
-1- FUNCTION: SOMATOSTATIN
-1- SUBCELLULAR LOCATION: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
336.33
336.33
336.33
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336.11
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09ygh5 carassius a
09ygh4 carassius a
P01171 ictalurus p
P87384 rana ridibu
                                                                                                                                March 21, 2003, 11:35:23; Search time 3.00429 Seconds (without alignments) 345.142 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
                                                                                                                                                                                                                                                                                                                                                                                                          112892
                   GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                           122
1 MRVSQIHCALALLGLALAICSOGAA 25
                                                                                                                                                                                                                                                                                                                                                               112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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aeropyrum p gallus gall homarus gam alligator m alligator m anas platyr gallus gall

mus musculu

sceloporus

Q9pvk2 P19140 P51913 Q9w710

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RESULT 2 SMSA_CARAU

o sapien musculu

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P40370 schizosacch 027655 fasciola he fasciola he bos taurus

schistosoma peal rattus norv gallus gall

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   basic residues; Hormone; Signal; Multigene family. 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-82265698; PubMed-6179939;
MITH C.D., Taylor W.L., Magazin M.D., Tavianini M.A., Collier K.J.,
Weith H.L., Dixon J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ictalurus punctatus (Channel catfish).
Ekkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae, Ictaluridae, Ictaluridae, Ictaluri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-82082515; PubMed-6171821;
Taylor W.L., Collier K.J., Deschenes R.J., Weith H.L., Dixon J.E.,
"Sequence analysis of a cDNA coding for a pancreatic precursor to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weith H.L., Dixon J.E.; The structure of cloned DNA complementary to catfish pancreatic
                                                       Otto C.J., Peter R.E.;
"The expression of SRF mkNA in the brain of goldfish.";
Submitted (SFP-1997) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7-1-101-1986 (Rel. 01, Created)
1-01-101-1990 (Rel. 15, Last sequence update)
16-0CT-2001 (Rel. 10, Last annotation update)
Somatostatin I precursor [Contains: Somatostatin-14 (SS-14)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 73; DB 1; Length 120;
Pred. No. 0.0009;
; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [TYR21,GLY24]SOMATOSTATIN-28.
[TYR7,GLY10]SOMATOSTATIN-14.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> RW (IN REF. 2).
98957D68011A651A CRC64;
                                                                                                                                                              -i- SUBCELLULAR LOCATION: Secreted.
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Proc. Natl. Acad. Sci. U.S.A. 78:6694-6698(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dixon.J.E., Andrews P.C.; "Somatostatins of the channel catfish."; Adv. Exp. Med. Biol. 188:19-29(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           somatostatin-14 messenger RNA.";
J. Biol. Chem. 257:10372-10377(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Somatostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-85303576; Pubmed-2863931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRVSQIHCALALLGLALAICSQGA 24
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Les 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR004250;
Pfam; PF03002; Somato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cleavage on pair of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
         SEQUENCE FROM N.A.
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P01171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of basic residues; Hormone; Signal; Multigene family. 24 POTENTIAL.
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
extinopteorygii, Neopterygii, Teleostei; Ostarlophysi; Cypriniformes;
Cyprinidae; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                 Lin X.-W., Peter R.E.; "Cloning and characterization of cDNAs encoding preprosomatostatin-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin X.-W., Peter R.E.; "Cloning and characterization of cDNAs encoding preprosomatostatin-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lunaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
                                                 16-OCT-2001 (Rel. 40, Created)
116-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Somatostatin IA precursor (Contains: Somatostatin-26; Somatostatin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. 40, Last sequence update)
1. 40, Last annotation update)
precursor (Contains: [Tyr21,Gly24]somatostatin-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                and -II from goldfish brain.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SOMATOSTATIN INHIBITS THE RELEASE OF SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL. SOMATOSTATIN-26 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY.
B5920015E2D272A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 74; DB 1; I
Pred. No. 0.00062;
; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOMATOSTATIN-14.
BY SIMILARITY.
   114 AA.
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   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12574 MW;
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llarity 64.0%;
Conservative
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es 16; Conserv
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                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                          Carassius auratus
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SMSA_CARAU
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DISULFID SEQUENCE Query Match

Matches

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Gaps

us-09-727-739b-19.rsp

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EMBL; Y00718; CAA68706.1; -.
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115 AA;
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for commercial
                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in on with modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
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                                         Kana ridibunda (Laughing frog) (Marsh frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
NCBL_TaxID=8406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWSI_RANRI STANDARD; PRT; 115 AA.
P87381, 095E18, 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Somatostatin 1 precursor (PSS1) [Contains: Somatostatin-14 (S-I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-97057290; PubMed-8901629;
Tostivint H., Lihrmann I., Bucharles C., Vieau D., Coulouarn Y.,
Fournier A., Conlon J.M., Vaudry H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fournier A., Conlon J.M., Vaudry H.;
"Occurrence of two somatostatin variants in the frog brain:
characterization of the CDNAs, distribution of the mRNAs, and
receptor-binding affinities of the peptides.";
Proc. Natl. Acad. Sci. U.S.A. 93:12605-12610(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.5%; Score 64; DB 1; Length 114; 52.0%; Pred. No. 0.017; 1ve 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E -> Q (IN REF. 2).
FEE0F2C76F74D99F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S00292; RIIDS1.
InterPro: IPP004280; Somatostatin.
Pfam; PP03002; Somatostatin; 1.
Cleavage on pair of basic residues; Hormone; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOMATOSTATIN-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MRVSQIHCALALLGLALAICSQGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HPSTRIQCALALLAVALSVCSVSGA 25
                                     PubMed-6114953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93038702; PubMed-1358069;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 AA; 12419 MW;
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M25903; AAA49339.1; -. EMBL; V00607; CAA23877.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 102-115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
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Matches
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οy qq

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03002; Somatostatin; 1.
Cleavage on pair of basic residues; Hormone; Multigene family; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- CATALYTIC ACTIVITY: 2-phospho-D-glycerate - phosphoenolpyruvate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1988 (Rel. 08, Created)
11-AUG-1988 (Rel. 08, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Enolase (EC 4 2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus
tochem. Biophys. Res. Commun. 188:477-482(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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MEDGINE-88268812; PubMed=3390159;
Segil N., Shrutkowski A., Dworkin M.B., Dworkin-Rastl E.;
Segil N., Shrutkowski A., Dworkin M.B., Dworkin-Rastl E.;
Enolase isoenzymes in adult and developing Xenopus laevis and characterization of a cloned enolase sequence.";
Blochem. J. 251:31-39(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.5%; Score 58; DB 1; Length 115; 56.0%; Pred. No. 0.12; vative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'SIMILARITY.
349756FEB4ABE213 CRC64;
                                                                                                   -1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - SUBUNIT: HOMODIMER.
-- SUBCELLULAR LOCATION: CYTOPLESMIC.
-- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (sor send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   interPro; IPR004250; Somatostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MOSCRVQCALTLLSLALAINSISAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MRVSQIHCALALLGLALAICSQGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12691 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC60093.1; -.
                                                               I - SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 56.0
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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NCBI_TaxID=8355;
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METAL
TRANSMEM
TRANSMEM
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SMS_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenselabseib.ch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions on its grant as its content is in no way
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-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
-1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE CYTOCHROME C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 54; DB 1; Length 433;
Pred. No. 1.4;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales; Desulfurococcacee; Aeropyrum.
NCBL_TaxID=56636;
                                                                                                                                                                                                                                                                                               BY SIMILARITY.

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

83C922489B530EB4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K1;
Wakagi T., Ishikawa R.;
Wakagi E. or Ishikawa R.;
Wamacoopper.oxidase.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-CCT-2001 (Rel. 39, Last sequence update) . Heme-copper oxidase subunit I+III (EC 1.9.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     815 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ropean Bioinformatics Institute.
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                                                                                                                                               Probom; PD000902; Enclase; 1:
TIGERAMS; TIGER01060; enc; 1.
PROSITE; PS00164; ENCLASE; 1.
Lyase; Glycolysis; Magnesium.
INIT_MET 0 0 0
INIT_MET 157 BY
METAL 244 244 MAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 39, Created)
(Rel. 39, Last seq
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                    4737.3 MW;
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PIR; S00463; NOXL.
HSSP, P56252; 1PDZ.
InterPro; IPR000941; Enolase.
Pfam: PF00113; enolase; 1.
PRINTS; PR00148; ENOLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 ANALLGVSLAVCKAGAA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 ALALLGLALAICSOGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                 244
292
317
433 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity es 11; Conserv
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30-MAY-2000 (
16-OCT-2001 (
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AOXI_AERPE
AC 30-MAY-2000
DT 30-MAY-2000
DT 16-OCT-2001
BE Heme-copper
GN AOXB OR ABOR
OC Archaea; Cre
CC Archaea; 
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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between
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Matches
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Gaps
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0c7-1993 (Rel. 27, Created)
1-0c7-1993 (Rel. 27, Last sequence update)
16-0c7-2001 (Rel. 40, Last annotation update)
Somatostatin precursor [Contains: Somatostatin-18; Somatostatin-14].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nate K., Kobayashi T., Karahashi K., Kato S., Yamamoto H.,
Yonekura H., Okamoto H.,
Submitted (JUN-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                      Copper; Transmembrane; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 815;
                                                                                                                                                                                                                                                                                                                                                 IRON (HEME A3) (PROBABLE) .
IRON (HEME A) (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
9E911C57BEF9BBE2 CRC64;
                                                                                                                                                                                                                                                            (PROBABLE)
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
POTENTIAL
POTENTIAL
                                                                   Pfam; PF00115; COX1; 1.
Pfam; PF00115; COX1; 1.
Pfam; PF00510; COX1; 1.
PRODOM; PD000382; CytC_OXdse_III; 1.
PROSTIE; PS00077; COX1; 1.
OXidoreductase; Heme; Copper; Transmem!
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EMBL; AP000060; BAA79771.1; ALT_INIT.

EMBL; PR0011, IFF.

InterPro; IPR000883; COXI.

InterPro; IPR000239; CytC_oxdse_III.
                                                                                                                                                                                                                                                                           COPPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90860 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMS_CHICK
P33094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRANSMEM
TRANSMEM
TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- COPACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                   DT 01-NOV-1995 (Rel. 32, Leated)
DT 01-NOV-1995 (Rel. 32, Leated)
DT 01-NOV-1995 (Rel. 32, Leat sequence update)
DT 01-NOV-1995 (Rel. 41, Leat annotation update)
DE 15-JUN-2002 (Rel. 41, Leat annotation update)
DE 91ycerate hydro-1yase) (Fragment)
DE 91ycerate hydro-1yase) (Fragment)
CS Alligator mississippiensis (American alligator)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
CC Archosauria; Grocodylidae; Alligatorinae; Alligator.
RN [1]
RN FEGUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular evidence for the origin of birds.";
Proc. Natl. Acad. Sci. U.S.A. 91:2621-2624(1994).
-1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1, Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42884 MW; B43E91228E9110B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - PATHWAY: Glycolysis.
- SUBUNIT: HOMODIMER (BY SIMILARITY).
- SUBCELLUIAR LOCATION: Cytoplasmic.
- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
MAGNESIUM (BY S
MAGNESIUM (BY S
MAGNESIUM (BY S
                                                                                                                                                       Mismatches
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42.6%; Score 52; Is Best Local Similarity 58.8%; Pred. No. 2 Matches 10; Conservative 4; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-94195794; PubMed-8146164;
                     METAL 319 319 M
SEQUENCE 433 AA; 47041 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom; PD000902; Enclase; 1.
TIGREAMS; TIGRO1060; enc; 1.
PROSITE; PS00164; ENOLASE; 1.
Lyase; Glycolysis; Magnesium.
Mon men
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L28078; AAA53671.1; -.
HSSP; P56252; 1PDZ.
                                                                                                                                                                                                                                                 107 ANAILGVSLAICKAGAA 123
                                                                                                                                                                                                   9 ALALLGLALAICSOGAA 25
                                                                                                                                                    Conservative
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                                                                                                Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                 ENO_ALLMI
P42897:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro
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                                                                                                                                                                                                                                                                                                                               RESULT 10.
ENO_ALLMI
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                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homarus gammarus (European lobster) (Homarus vulgaris).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Nephropoldea; Nephropidae; Homarus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      querroy S., Camus C., Janin J.;

ray structure and catalytic mechanism of lobster enclase.";

tochemistry 34:12513-12523(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- COPACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
43.4%; Score 53; DB 1; Length 116;
Best Local Similarity 52.4%; Pred. No. 0.63;
Matches 1; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                PIN: "SZUDSU, SZUCJU,
DERONAL SZUCJU,
DERONAL DERONALOSTATIO.
DERONAL SIGNAL
SIGNAL
SIGNAL
1 24 BF SIMILARITY.
DEPTIDE 29 BR SIMILARITY.
DEPTIDE 103 116 SOMATOSTATIN-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                            89 116 SOMATOSTATIN-28
103 116 SOMATOSTATIN-14
105 116 WW: 8A5BB9BDA8A291BA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
-1- SIMILARITY: BELONGS TO THE SOMATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- PATHWAY: Glycolysis.
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SUBCELLUAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
PDB: 1PDY; 14-NOV-95.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE~96038209; PubMed-7547999;
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; TIGR01060; eno; 1.
PS00164; ENOLASE; 1.
ilycolysis; Magnesium; Ace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IA-NOV-95.
InterPro; IRR000941; Enclase.
Pfam; PF00113; enclase, I.
PRINTS; PR00148; ence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 QIHCALALLGLALAICSQGAA 25
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P56252;
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us-09-727-739b-19.rsp

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(Phosphopyruvate
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     NCBI_TaxID=8839
                                                                                                                                                                                                                                                                                                                                                                THE DIMER
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P51913:
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INIT_MET
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha enclase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (Tau-
                                                                                                                                                                                                    .....yducor mississippiensis (American alligator).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Crocodylidae; Alligatorinae; Alligator.
                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo:
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Length 433;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD3DD59FB1EBB3DA CRC64;
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TIGREAGE, TIGREAGE, 1.
LYASE, Glycolysis; Magnesium; Multigene family.
Lyase, Glycolysis; Magnesium; Multigene family.

NAMAGNESIUM (BY SIMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: CYTOPIASMIC.
                                                    433 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 1
Pred. No. 2.7;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- PATHWAY: Glycolysis.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99439677; PubMed=10508547;
Mannen H., Li S.S.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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01-NOV-1990 (Rel. 16, Last sequ
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ilarity 58.8%;
Conservative
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west Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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ENOA_ANAPL
ID ENOA_ANAPL
AC P19140;
DT 01-NOV-1990
DT 15-JUN-2002
DT 15-JUN-2002
DE CYSTALLIIN).
OC ALCHORGE;
OC ALCHORGEIT;
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RESULT 11
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(See http://www.isb-sib.ch/announce,
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                                                                                                                                                                                                                                                                            H(2)O.
-1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                      lens structural protein.";
J. Cell Biol. 107:2729-2736(1988).
-!- FUNCTION: BOTH AN ENZYME AND A LENS STRUCTURAL PROTEIN.
-!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate
                                                  Wistow G.J., Lietman T., Williams L.A., Stapel S.O., de Jong W.W., Horwitz J., Piatigorsky J.; "Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0c7-1996 (Rel. 34, Created)
01-0c7-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)
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MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

MAGNESIUM (BY SIMILARITY).

4: laed78b08a66e84D CRC64;
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Glycolysis; Magnesium; Eye lens protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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IISSUE-Embryonic lens;
MEDLINE-89079778; PubMed-2462567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 292 N
317 317 M
433 AA; 47108 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000941; Enolase.
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Best Local Similarity .58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               robom; PD000902; Enclase;
IGRFAMs; TIGR01060; enc; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M20749; AAA49218.1;
EMBL; X14195; CAA32409.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 ALALLGLALAICSOGAA 25
                                                                                                                                                                                                                                                                                                                                                                  -i- PATHWAY: Glycolysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A32132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration to between the Swiss Institute of Bioinformatics and the EMBL outstainnter European Bioinformatics and the EMBL outstainnter European Bioinformatics Institute. There are no restrictions on its cuse by non-profit institutions as long as its content is in no way conditied and this statement is not removed. Usage by and for commercial corrections of incense agreement (See http://www.isb-sib.ch/announce/corrections and nemail to license@isb-sib.ch).

EMBL: AF072589; AAD41646.1;

EMBL: AF072589; AAD41646.1;

EMBL: AF072589; ABD41646.1;

EMBL: AF0725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed as its concert is in no way entities requires a license agreement (see http://www.isp-sib.ch/announce/commercial).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Muscle;
TISSUE-Muscle;
MEDLINE-9943967;
Mannen.H., Li S.S.-L.;
"Molecular evidence for a clade of turtles.";
Mol. Phylogenet. Evol. 13:144-148(1999).
"CATALITIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Alpha enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase)
Sceloporus undulatus (Eastern fence lizard) (Skink)
Eukaryota; Metazoa; Ohordate; Cranlata; Vertebrata; Euteleostomi; Sceloporus.
Sceloporus.
(NCBL_TaxID-8520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.6%; Score 52; DB 1; Length 433; 58.8%; Pred. No. 2.7; ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       im; Multigene family.
BY SIMILARITY.
MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
MAGNESIUM (BY SIMILARITY)
(W): EOAD198562629033 CRC64;
                                                         -- SUBCNIT: HOMODIMER (BY SIMILARITY)
-- SUBCELLULAR LOCATION: CYCOPISSMIC
-- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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METAL 292 292 MA
METAL 317 317 SEQUENCE 433 AA; 47439 MW;
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Q9W7L2;
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les 10; Conserret
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Best Local S
Matches 10
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                                                                                                                                                                                                                                                                                                       COFACTOR: MAGNESTUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
COFACTOR: MAGNESTUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
COFACTOR: Glycolysis.
COFACTOR: Glycolysis.
COFACTOR: CATOR: Cytoplasmic.
COFACTOR: CYTOPLA.
COFACTOR.
COFACTOR: CYTOPLA.
COFACTOR: CYT
                                                                                                                                                                                   J. Biochem. 117.554-559(1995).
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THE DIMER (BY SIMILARITY).
-1- PATHWAY: Glycolysis.
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nucleotide sequence
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Alpha enolase (Rel 41, List annotation update)
Alpha enolase (Rel 42, Lill) (2-phospho-D-glycerate hydro-lyase)
Python regius (Ball python) (Royal python)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Pythonidae; Python
VCBI_TaxID=51751;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42.6%; Score 52; DB 1; Length 433; 58.8%; Pred. No. 2.7; Live 4; Mismatches 3; Indels 0;
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MAGNESIUM (BY SIMILARITY).
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93ADGB0A7AD99910 CRC64;
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Tanaka M., Maeda K., Nakashima K.;
"Chicken alpha-enolase but not beta-enolase has
tyrosine-phosphorylation site: CDNA cloning and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENOA PYTRG STANDARD; PRT; 433 AA.
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292 292 MAG
317 317 MAG
433 AA; 47173 MW; §
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107 ANAILGVSLAVCKAGAA 123
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les 10; Conservative
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	EMBL; AF072587; AAD41644.1; SSSP; P65252; 1PD2.1 Interprovements of the provention of the provents of the p	Prant Pro0113; brootase; 2. PRINTS; PR00148; ENOLASE.	ProDom; PD000902; Enolase; 1. TICRFAMS, TICRO1060; eno; 1. DPORTUP: DEADLASE ENDIASE: 1	Lyase; Glycolysis; Magnesium; Multigene family. INIT_MET 0 0 0 BY. SIMILARITY.	METAL 244 244 MAGNESTUM (BY SIMILARITY) METAL 292 292 MAGNESTUM (BY SIMILARITY) METAL 317 MAGNESTUM (BY SIMILARITY) SEQUENCE 433 Aa; 47362 MW; 7CD89EB405529301 GRC64;	Ouery Match 42.6%; Score 52; DB 1; Length 433; Best Local Similarity 58.8%; Pred. No. 2.7; Matches 10; Conservative 4; Mismatches 3; Indels	9 ALALLGLALAICSOGAA 25 : : : 107 ANAILGVSLAVCKAGAA 123
<u>ر</u> ز	2222	DR B	D R C	FT	FT FT SQ	O M W	y 0,

Search completed: March 21, 2003, 11:38:45 Job time : 5.00429 secs

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C; Accession: 151064
M. A. Moore, C.A.; Kittilson, J.D.; Dahl, S.K.; Sheridan, M.A.
Gen. Comp. Endocrinol. 98, 253-261, 1995
A; Pitle: Isolation and characterization of a cDNA encoding for preprosomatostatin c
A; Reference number: 151064; MUID: 95354921; PMID: 7628684
phosphopyruvate hy phosphopyruvate hy CT481 hypothetical conserved hypothet pilus assembly pro probable membrane-phosphopyruvate hypothetical prote hypothetical prote phosphopyruvate hy hypothetical prote hypothetical prote hypothetical prote hypothetical prote
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hypothetical prote
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C.Species: Oncorhynchus.mykiss (rainbow trout)
C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Gross-references: EMBL:U32471; NID:9975344; PIDN:AAC59695.1; PID:9975345
C;Superfamily: somatostatin
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Pred. No. 8.1e-09;
2; Mismatches 1; Indels
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A;Molecule type: mRNA
A;Residues: 1-115 <MOO>
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ilarity 88.0%;
Conservative
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Matches
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somatostatin-14 pr
                                                                                                                                 March 21, 2003, 11:38:56; Search time 5.36481 Seconds (without alignments) 447.986 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                           GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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122
1 MRVSQIHCALALLGLALAICSQGAA 25
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                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum Match 100
Listing first 45
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length: 2000000000
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Match
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Perfect score:
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Maximum DB seq
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NiAlternate names: somatostatin I NiAlternate names: somatostatin I Ciontains: somatostatin 14 Ciontains: somatostatin 14 Cipate: 30-Jun-1980 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999 Cipate: 30-Jun-1980 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999 Cipate: 30-Jun-1980 #sequence_revision 31-Dec-1993 #text_change 18-Jun-1999 Rightin, C.D.; Taylor, W.L.; Magazin, M.; Tavianini, M.A.; Collier, K.; Weith, H.L. J. Biol. Chem. 257, 10372-10377, 1982 A; Fitle: The structure of cloned DNA complementary to catfish pancreatic somatostat A; Reference number: S00292; MUID:82265698; PMID:6179939 of a cDNA coding for a pancreatic precursor to somatosta MUID:82082515; PMID:6171821 A; Residues: 1.114 < RINS
A; Cross-references: EMBL:V00607; NID:964017; PIDN:CAA23877.1; PID:964018
A; Cross-references: EMBL:V00607; NID:964017; PIDN:CAA23877.1; PID:964018
B; Taylor, W.L.; Collier, K.J.; Deschenes, R.J.; Weith, H.L.; Dixon, J.E. Proc. Natl. Acad. Scil. U.S.A. 78, 6694-6698, 1981
A; Title: Sequence analysis of a cDNA coding for a pancreatic precursor to A; Reference number: A93897; MUID:82082515; PMID:617821 ecursor - channel catfish somatostatin I somatostatin-14 precursor Molecule type: mRNA

phosphopyruvate hy hypothetical prote

somatostatin-14 prohosphopyruvate hy

cytochrom

omatostatin

preprosomatostatin

Molecule type: mRNA Residues: 82-108 <TAX> Cross-references: GB:J00944 Andrews, P. C.; Dixon, J.E. Biol. Chem. 256, 8267-8270, 1981

R; Andrews,

pothetical prote robable binding p

pothetical prote

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C.Accession: $00463
R.Segli, N.; Shrutkowski, A.; Dworkin, M.B.; Dworkin-Rastl, E.
Blochem. J. 211, 31-39, 1988
A.Title: Enolase isoenzymes in adult and developing Xenopus laevis and characterizati
A.Reference number: $00463; MUID:88268812; PMID:3390159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to p A;Pathway; glucomogenesis; glycolysis C;Superfamily: enolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Keywords: Carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis; hydro-lyase; mag
f.40/binding site: magnesium 2 (Ser) #status predicted
F.210, 343/Active site: Glu, Lys #status predicted
F.245, 293, 318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable cytochrome-c oxidase (EC 1.9.3.1) chain I APE0793 - Aeropyrum pernix (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rikawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawawa, H.; Takamiya, T.; Takamiya, T.; Tahamiya, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-818 <KAW>
A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79771.1; PID:g5104456
                                                                                                                                                                                                           phosphopyruvate hydratase (EC 4.2.1.11) ENO1 - African clawed frog A.A.Hernate names: enolase ENO1
C.Species: Xenopus laevis (African clawed frog)
C.Species: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Superfamily: cytochrome-c oxidase chain I/III; cytochrome-c oxidase chain C; Keywords: copper; electron transfer; heme; iron; magnesium; membrane-ass F; 73, 380 Fainding site: heme a iron (His) (axial ligands) #status predicted F; 251, 300, 301/Binding site: copper (His) #status predicted E; 251-255/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-434 <SEG>
A;Cross-references: EMBL:Y00718; NID:g64679; PIDN:CAA68706.1; PID:g64680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F:255/Binding site: oxygen (Tyr) #status predicted
F:386/Binding site: heme a3 iron (His) (axial ligand) #status predicted
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4: Mismatches
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Pred. No.
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                                                  Match 44.3%;
Local Similarity 64.7%;
les 11; Conservative
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ilarity 52.2%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 ANALLGVSLAVCKAGAA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 ALALLGLALAICSOGAA 25
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-818 <K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                            RESULT 5
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v. Accession: JC6166
F. Tostivint, H. Lihrmann, I.; Bucharles, C.; Vieau, D.; Coulouarn, Y.; Fournier, A.; Cd Proc. Natl. Acad. Sci. U. S.A. 93, 12605-12610, 1996
A. Title: Occurrence of two somatostatin variants in the frog brain: Characterization of A. Title: Occurrence of two somatostatin variants in the frog brain: Characterization of A. Contents: brain
A. Contents: brain
A. Accession: JC6166
A. MUID: 97057290; PMID: 8901629
A. Contents: brain
A. Residues: 1-115 < TOS
A. Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone. C. Genetics:
C. Comment: This protein acts both as a neurotransmitter/neuromodulator and a hormone. C. Genetics:
C. Superfamily: somatostatin
C. Keywords: brain; hormone
          sequence. A
A; Title: Isolation and structure of a peptide hormone predicted from a mRNA shefetence number: A92334; MUID:81264223; PMID:6114953
A; Reference number: A92334
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 10-114 <AND
C; Superfamily: somatostatin
C; Superfamily: somatostatin
F; 1-24Domain: signal sequence #status predicted <SIG>
F; 5-100/Domain: propeptide #status predicted <PRO>
F; 101-114/Product: somatostatin-14 #status experimental <AMT>
F; 103-114/Disolifide bonds: #status experimental <AMT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternate names: PSS1 protein
Species: Rana ridibunda (laughing frog)
Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Ictalurus punctatus (channel caffish)
Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
Accession: IS0798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 114; 0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 64; DB 2; Length 114;
Pred. No. 0.036;
5; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.5dte: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text C;Accession: 150798
R:Dixon, J.E.; Andrews, P.C.
Adv. Exp. Med. Biol. 188, 19-29, 1985
A;Title: Somatostatins of the channel catfish.
A;Reference number: 150798, MUD:85303576; PMID:2863931
A;Accession: 150798
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 114 4017.
A;Kesidues: 1-114 4017.
A;Crosr-references: GB:M25903; NID:g213339; PIDN:AAA493
C;Superfamily: somatostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Iv. Exp. Med. Biol. 188, 19-29, 1985
Title: Sometostatins of the channel catfish.
Reference number: I50798; MUID:85303576; PMID:2863931
Accession: 150798
                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.0
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          Score 64;
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Pred. No.
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protein
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52.0%;
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llarity ,52.0%;
Conservative
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les 13; Conserv
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Tostivint, H.; Lih
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Best Local 8
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Gaps

3; Indels

....ynesium; membrane associated com ligands) #status predicted predicted [8-70...

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Gaps

7; Indels

DB 2; Length 818;

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NiAlternate names: enolase gamma; neuron-specific enolase
(Sispecies: Homo saptens (man)
(Man
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-434 <OL1>
A:Cross-references: GB:M22349; NID:g951199; PIDN:AAB59554.1; PID:g182116; GB:M27833
R:Ol1va, D: Cali, L: Feo, S.; Giallongo, A.
Genomics 10, 157-165, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 05-Aug-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A;Residues: 2-3,'Q',5-239,'M',241-434 <MCA>
A;Cross-references: EMBL:X13120; NID:g31145; PIDN:ÇAA31512.1; PID:g930063
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R;McAleeee, S.M.; Dunbar, B.; Pothergill, J.E.; Hinks, L.J.; Day, I.N.M.
Eur. J Blochem. 178, 413-417, 1988
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Pred. No. 5.7;
                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Chin, C.C.C.
J. Protein Chem. 9, 427-432, 1990
A;Title: The primary structure of rabbit muscle enclase.
A;Reference number: A37210; MUID:91113295; PMID:2275753
A;Accession: A37210
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                                                                                     DB 2;
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                                                                                                                                                                                     4; Mismatches
     C; Keywords: carbon-oxygen lyase; hydro-lyase
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                                                                                          42.6%;
58.8%;
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                                                                                Query Match
Best Local Similarity 58.8%
Matches 10; Conservative
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Best Local Similarity 58.89
Matches 10; Conservative
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A; Residues: 1-434 <OL2>
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Freuers. 5-1.

From Natl. Acad. Sci. U.S.A. 91, 2621-2624, 1994

A.Title: Molecular evidence for the origin of birds.

A.Title: Molecular evidence for the origin of birds.

A.Reference number: A53470; MUID:94195794; PMID:8146164

A.Accession: 150026

A.Status: preliminary: nucleic acid sequence not shown; translation not shown; translation a.Molecule type: mRNA

A.Molecule type: mRNA

A.Residues: 1-395 <HED>

A.Cross-references: GB:L28078; NID:9472796; PIDN:AAA53671.1; PID:9472797

S.Superfamily: enolase

C.Keywords: carbon-oxygen lyase; hydro-lyase
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C; Species: Pasciola hepatica (liver fluke)
C; Date. 07-0ct-1994 #sequence_revision 07-0ct-1994 #text_change 22-Jun-1999
C; Accession: A53665
R; Davis, R.E.; Singh, H.; Botka, C.; Hardwick, C.; Ashraf el Meanawy, M.; Villanueva, J. J. Biol. Chem. 269, 20036-20030, 1994
A; Title: RNA trans-splicing in Fasciola hepatica. Identification of a spliced leader (Si A; Accession: A53665; MUID:94327554; PMID:8051087
                                                                                                                                                                                                                                                                                                                                                 C; Accession: $20630
R; Nata, K.; Kobayashi, T.; Karahashi, K.; Kato, S.; Yamamoto, H.; Yonekura, H.; Okamoto,
submitted to the EMBL Data Library, June 1991
A; Description: Nucleotide sequence determination of chicken somatostatin precursor cDNA.
A; Reference number: $20630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphopyruvate hydratase (EC-4.2.1.11) alpha - American alligator (fragment)
                                                                                                                                                                                                                                                           Species: Gallus gallus (chicken)
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Alligator mississippiensis (American alligator)
;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 22-Jun-1999
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.species: Fasciola hepatica (liver fluke).
.bate: 07.0ct-1994 #sequence_revision 07.0ct-1994 #text_change 22-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V:Cross-references: EMBL:X60191; NID:962985; PIDN:CAA42747.1; PID:962986 - C:Superfamily: somatostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:U10297; NID:9499266; PIDN:AAA57450.1; PID:9499267 C;Superfamily: enolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
43.4%; Score 53; DB 1; Length 116;
Best Local Similarity 52.4%; Pred No 1.4;
Matches 11; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 395;
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Pred. No. 5.3;
418 RLGKIHFALAMLGVALTFLPQFA 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 QIHCALALLGLALAICSQGAA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: alpha-enolase
                                                                                                                                                                                                                        omatostatin precursor - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86 ANAILGVSLAVCKAGAA 102
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Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-116 <NAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <DAV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Alligator
C; Date: 21-Feb-1997 #
C; Accession: 150026
R; Hedges, S.B.
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Gaps

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Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Pathway: gluconeogenesis; glycolysis
C; Superfamily: enclase
C;Keywords: carbon-carbon lyase; carbon-oxygen lyase; dimer; gluconeogenes
C;Keywords: carbon-tarbon lyase; carbon-oxygen lyase; dimer; gluconeogenes
F;40/Binding site: magnesium 2 (Ser) #status predicted
F;210,343/Active site: Glu, Lys #status predicted
F;245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted
                                                                                     NID:g50143; PIDN:CAA44540.1; PID:g50144
c, S.; Lucas, M.; Keller, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
Molecule type: mRNA
Residues: 59-233, NA',236-434 <LA2>
Gross-references: 6B:M20745; NID:9193029; PIDN:AAA37554.1; PID:9387144
Experimental source: skeletal muscle
                                                                                                                                                                                                                                                                                                                                                              Cross-references: EMBL:X57747; NID:950846; PIDN:CAA40913:1; PID:950847
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title: Murine muscle-specific enclase: CDNA cloning, s
Reference number: A33921; MUID:89282789; PMID:2734297
                                                                                                                        zar, M.; Lamande, N.; Brosset, S.; Lucas, M.;
litted to the EMBL Data Library, February 1991
ference number: $29675
cession: $29675
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Pred. No. 5.7;
4; Mismatches
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                                                                                             EMBL: X62667;
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Best Local Similarity 58.8
Matches 10; Conservative
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                                                          1-434 <PET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lecule type: DNA
sidues: 1-28 <SA2>
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                                                                                                                                                                                                                                                            preliminary
                                                                                             coss-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: A33921
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R; Sakimura, K.
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C:Superfamily: enolase
C:Superfamily: enolase
C:Reywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolysis;
F:2-43/Foroluct: phosphopyruvate hydratase gamma #status predicted <AMT>
F:2-Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #status
F:40/Binding site: magnesium 2 (Ser) #status predicted
F:20,343/Active site: Glu, Lys #status predicted
F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted
J. Neurosci. Res. 19, 450-456, 1988
A/Filte: Human gamma enolase: isolation of a cDNA clone and expression in normal and tun
A/Reference number: I56569; MUID:88259288; PMID:3385803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:Y00691; GB:M27610
R;Harington'C.R.; Oblin, GB.; Hurt, J.; Day, I.N.M.; Wischik, C.M.
Biophys. Acta 1158, 1262-128, 1993
A;Title: Characterisation of an epitope specific to the neuron-specific isoform of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phos
A.Pathway: gluconeogenesis; glycolysis
                                                                                                                                                                                                                                                                                                                                                                                                 neurone-specific enolas
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He EMBL Data Library, October 1991
Beta-enolase: a gene expressed in undifferentiated postnatal myoblasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma) in
le ions of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ta, and gar
                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 'GC', 29-126, 'N', 128-434 < VAN>
A; Cross references: GB:M36766; NID:g182117; PIDN:AAA52388.1; PID:g182118
R; Day, IN. M.; Allsopp, M.T.E.P.; Moore, D.C.M.; Thompson, R.J.
FBS Lett. 222, 139-143, 1987
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A; Residues: 1-434 CLAN>
A; Residues: 1-434 CLAN>
A; Cross-references: EMBL: X61600; NID: 950848; PIDN: CAA43797.1; PID: 950849
R; Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M.
submitted to the EMBL Data Library, October 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: 12p13-12p13
A;Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               beta,
to ch
                                                                                                                                                                                                                                                                                                                                                                             Title: Sequence conservation in the 3'-untranslated regions of Reference number: S02616; MUID:88005129; PMID:3653393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comment: Enclase occurs with at least three isoforms (alpha, Comment: Thr-191 may be important for the enhanced tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 52; DB 1; Length 434;
Pred. No. 5.7;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of beta/A4-protein.

Seference number: $38303; MUID:94002176; PMID:7691181
Accession: $38303; MUID:94002176; PMID:7691181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      not compared with conceptual translation
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C; Species: Mus musculus (house
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 ALALLGLALAICSQGAA 25
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Matches
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dimer; gluconeogenesis; glycoly

DB 1; Length 434;

sequence, and developmental

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phosphopyruvate hydratase (EC 4.2.1.11) gamma - rat
N:Alternate names: 2-phospho-glycerate dehydratase; enolase gamma; neuronal enolase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 22-Jun-1999
C;Accession: A24742; P00006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:M22770; GB:M18742; NID:9205766; PIDN:AAA41725.1; PID:9554480
                                                                                                                                                                                                                                        R;Sakimura, K.; Kushiya, E.; Obinata, M.; Odani, S.; Takahashi, Y.
Proc. Natl. Acad. Sci. U.S.A. 82, 7453-7457, 1985
A;Title: Molecular cloning and the nucleotide sequence of cDNA for neuron-specific A;Reference number: A24742, MUID:86042683; PMID:2865729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M11931; NID:g204041; PIDN:AAA41119.1; PID:g204042 R;Sakimura, K.; Kushiya, B.; Takahashi, Y.; Suzuki, Y. Gene 60, 103-113, 1987 1987 1987 1987 1987 1987 1988152493; PMID:2450052 A;Reference number: PQ0006; MUD:88152493; PMID:2450052
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Pred. No. 5.7;
1; Mismatches
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.J.; Lietman, T.; Williams, L.A.; Stapel, S.O.; de Jong, W.W.; Horwitz, J.; F. I. 107, 2729-2736, 1988 u.crystallin/alpha-enclase: one gene encodes both an enzyme and a lens struct number: A92750; MUID:89079778; PMID:2462567.
                                                                                                                                                                             Dumont, X.; Chalon, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; Res. 18, 3638, 1990
                                                                                                                                                                                                                            Nucleotide sequences of cDNAs alpha and gamma enclase mRNAs from mouse brain.
nce number: S10246; MUID:90301487; PMID:2362815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anas platyrhynchos (domestic duck)
-May-1990 #sequence_revision 21-May-1990 #text_change 21-Jul-2000
                                                                                                                           #sequence_revision 12-Feb-1993 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Resdudes: 1-434 <KAG>
A;Cross-Teferences: EMBL:X52380; NID:955494; PIDN:CAA36606.1; PID:955495.
;;Superfamily: enolase
C;Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase
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A/Residues: 1-434 <MIS>
A/Cross-references: GB:X14195; NID:g62455; PIDN:CAA32409.1; PID:g62456
A/Cross-references: GB:X14195; NID:g62455; PIDN:CAA32409.1; PID:g62456
S/Superfamily: enolase
S/Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase
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                                                 .2.1.11) gamma - mouse
cerate dehydratase; enolase gamma
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Pred. No. 5.7;
4; Mismatches
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Pred. No. 5.
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Best Local Similarity 58.8%;
Matches 10; Conservative
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Best Local Similarity 58.8
Matches 10; Conservative
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RESULT 14
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Search completed: March 21, 2003, 11:41:45 Job time: 7.36481 secs sedineuroe sedineuroe

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US-10-174-590-354
US-10-175-73-354
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US-10-173-706-354
US-10-175-75-35-354
US-10-176-482-354
US-10-176-913-354
US-10-176-913-354
US-10-176-913-354
US-10-176-913-354
US-10-174-579-354
US-10-174-579-354
US-10-174-588-354
US-10-175-739-354
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Publication No Presonandaesa
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                                                                                                                            March 21, 2003, 11:53:33 ; Search time 4.82833 Seconds (without alignments) 276.816 Million cell updates/sec
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                   GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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122
1 MRVSQIHCALALLGLALAICSQGAA 25
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match
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ALIGNMENTS

; Publication No. US20030044892A1
; GENERAL INFORMATION: . additions Rristal Augus Gruibh Company
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY6, EXPRESSE
; FILE REFERENCE: D0040NP/3053-4119US3
APPLICATION NU
CURRENT FILING DATE: 2002-05-07
FILE APPLICATION NUMBER: 60/235,602
FAIOR FILING DATE: VOUC.09-Z/
; PRIOR FILING DATE: 2001-08-28
, NUMBER OF SEQ ID NOS: 81
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 1582
. ; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-UY-960-422B-11
41.0%; Score 50;
cal Similarity 50.0%; Pred. No. 51;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 3 VSOIHCALALLGLALAIC 20
Db 910 VSTIGCALSIVCLALSVC 927
RESULT 2
US-09-796-692-2277
; Sequence 2277, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
G
Algate, F
APPLICANT: Mannion, Jane

Sequence 11, Appl Sequence 227, Ap Sequence 2342, Appl Sequence 9, Appl 1 Sequence 17, Appl Sequence 10, Appl Sequence 2, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 13, Appl Sequence 2, Appl 1 Sequence 2, Appl 1

US-09-843-164-10 US-09-843-164-8 US-09-843-164-14

US-09-84 US-09-84 US-09-84 US-09-971

Description

Length DB

Score

Sequence 5, A Sequence 5, A Sequence 44, Sequence 207,

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0; Gaps
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Pred. No. 11;
4; Mismatches 3; Indels
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27;
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NVENTION: Biochemical Markers for the Human
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-09-06
                                                                                                                                                                                                                                                                                                                                                   - Any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER: PCT/GB97/02394: 1997-09-05
                                                                                    NUMBER: 60/218,950
                                                                                                                   NUMBER: 60/222,903
: 2000-08-03
                                                                                                                                                 NUMBER: 60/223,416
: 2000-08-04
 60/200,999
                              7202,084
                                                            NUMBER: 60/206,201
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Best Local Similarity 56.2%;
Matches 9; Conservative
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Best Local Similarity 56.2%;
Matches 9; Conservative
                                                                          -05-22
                                              -02-04
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US-09-796-692-2342
                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens FEATURE:
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ORGANISM: Homo sapiens
US-09-935-642-9
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                                                                                                                                                                                                                                                                                                                    NAME/KEY: variant
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US-09-935-642-9
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TIE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TIE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY INVENTION: HEMATOLOGICAL MALIGNANCIES
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39.3%; Score 48; DB 9; Length 120;
Best Local Similarity 56.2%; Pred No. 7.9;
Matches 9; Conservative 4; Mismatches 3; Indels
Matches 9; Conservative 4; Mismatches 3; Indels
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25: 2077.001200
ICATION NUMBER: US/09/796,692
NG DATE: 2001-03-01
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SOFTWARE: FastSEQ for Windows Version 3.0
                                              us/09/796,692
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: 2000-03-17
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US-09-796-692-2277
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US20020061556Alel Human Membrane Proteins and Polynucle
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                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                      DB 10; Length 481;
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                                                                           Query Match 38.5%; Score 47; Best Local Similarity 45.0%; Pred. No. 4 Matches 9; Conservative 5; Mismatch
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 45.0%; Pred. No.
Matches 9; Conservative 5; Mismatc
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200 LSNVGCALSVTGLALTVIFQ 219
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142 LSNVGCALSVTGLALTVIFQ 161
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PRIOR FILING DATE: 2000-04-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Walke, D. Wade
                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: homo sapiens
US-09-843-164-8
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ORGANISM: homo sapiens
US-09-843-164-14
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                                                                                                                                                                                                                                                                        ION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1771;
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NESCH. 164-10
(NS-09-843-164-10
; Sequence 10, Application US/09843164
: Patent No. US20020061556Al
Sequence 17, Application US/10184644 Publication No. US20030044930A1
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Db 142 LSNVGCALSVTGLALTVIFQ 161
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Best Local Similarity 45.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                        Godowski, Paul J.
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 07705.0014-0
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2001-0
                                                                                                                                                                                                                                                                                                               FILE REFERENCE: P3430R1C227
                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER CURRENT FILING DATE: 2002-
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                                                                                                                                                                                                                                                                                                                                                                        Prior Application removed
NUMBER OF SEQ ID NOS: 612
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; ORGANISM: homo sapiens
US-09-843-164-10
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CORGANISM: Homo Sapien
US-10-184-644-17
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No. US20020061556Alel Human Membrane Proteins and Polynucleoti
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Rigel Pharmaceuticals, Incorporated
FAUTON: EDG: Modulators of Lymphocyte Activation and Migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
38:5%; Score 47; DB 10; Length 84%;
Best Local Similarity 45:0%; Pred No. 72;
Matches 9; Conservative 5; Mismatches 6; Indels
Matches 9; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 400;
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Pred. No. 48;
3; Mismatches
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FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                NUMBER: US/09/843,164
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US20020155512A1
                                                                                                                                                               Sequence 6, Application US/09843164
Patent No. US20020061556A1
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60.

PRIOR FILING DATE: 1000 04 27.

NUMBER OF SEQ ID NOS: 19.

SOFTWARE: FastSEQ for Windows V. SEQ ID NO 8.

LENGTH: 848
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488 LSNVGCALSVTGLALTVIFQ 507
                                                           488 LSNVGCALSVTGLALTVIFQ 507
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50.08;
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Masuda, Esteban
Chu, Peter
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Best Local Similarity 50.0
Matches 8; Conservative
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PRIOR FILING DATE: 2001-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: homo sapiens
US-09-843-164-6
                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 0770 CURRENT APPLICATION CURRENT FILING DATE:
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SOFTWARE: PatentIn
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                                                                                                                                                                 Length 560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB
Pred. No. 66;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEO ID NOS: 19
FastSEO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                         Application US/09843164
20020061556A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09843164 atent No. US20020061556A1
                                                                                                                                                               Query Match
Best Local Similarity 45.0%; Pr
Matches 9; Conservative 5;
                                                                                                                                                                                                                                                                            200 LSNVGCALSVTGLALTVIFQ 219
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200 LSNVGCALSVTGLALTVIFQ 219
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                               3 VSQIHCALALLGLALAICSQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VSQIHCALALLGLALAICSQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 38.5%;
Best Local Similarity 45.0%;
Matches 9; Gonservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 38.5
Best Local Similarity 45.(
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang, Xiaoming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: homo sapiens
US-09-843-164-2
                                                                                                   ; ORGANISM: Homo sapiens
US-09-966-4228-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: homo saplens
US-09-843-164-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION CURRENT FILING DATE:
                                        SEQ ID NO 2
LENGTH: 560
                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF
SOFTWARE:
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Sphingolipid Compositions and Methods for Their Therapeutic Use
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Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Indels
                                                                                                                                                                            I: Nabil A. Elshourbagy
INVENTION: RAT G-PROTEIN COUPLED RECEPTOR AXOR29
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 37.7%; Score 46; DB Best Local Similarity 50.0%; Pred. No. 48; Matches 8; Conservative 3; Mismatches
                                                                                                                                                                                                                          LICATION NUMBER: US/09/812,272
ING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER: US/10/037,616: 2002-04-19
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DATE: 2000-10-27
                                                                                                                                                                                                                                                           VUMBER: 60/191,153
2000-03-22
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US20020123148A1
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Best Local Similarity 50.0%;
Matches 8; Conservative
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; ORGANISM: Rattus norvegicus
US-10-037-616-27
Db 195 LFCVLAFLGILAAICA 210
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195 LFCVLAFLGILAAICA 210
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                                                                                                                                                                                                                                                                                                                              | SEQ ID NO 2
| LENGTH: 400
| TYPE: PRT
| ORGANIEM: HOMO SAPIENS
| US-09-812-272-2
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Search completed: March 21, 2003, 11:56:32 Job time : 5.82833 secs

Scoring table:

Searched:

Database

score:

Perfect son Sequence:

Title:

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Run on:

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Sequence 13, Assequence 9, Assequence 18, Assequence 4, Assequence 2, Assequence 2, Assequence 4, Assequence 6, As
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: W. HONG
APPLICANT: W. HONG
APPLICANT: Bruno. Sandra A.
APPLICANT: Elsenboss, Laura A.
APPLICANT: Elsenboss, Laura A.
APPLICANT: Elsenboss, Laura A.
APPLICANT: Cohan, Wichael
APPLICANT: Cohan, Victoria L.
APPLICANT: Bandman, Olga
FILE REFERENCE: PF-0458-1 CIP
CURRENT APPLICATION HUMBER: 09/09/705,448
CURRENT FILING DATE: 1908-07-16
PRIOR APPLICATION NUMBER: 09/116,641
PRIOR APPLICATION NUMBER: 09/008,271
PRIOR STLING DATE: 1998-07-16
PRIOR APPLICATION NUMBER: 09/008,271
PRIOR STLING DATE: 1998-01-16
PRIOR STLING DATE: 1998-01-16
NUMBER OF SEO ID NOS: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                               US-08-954-69
US-09-293-50
US-08-957-287
US-08-948-99
US-09-348-81
US-09-817-18
US-09-817-18
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LCGATION: 322
OTHER INFORMATION: 2435410, EOSINOT03
US-09-705-448-3
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Patent No. 6225103
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                          March 21, 2003, 11:41:02 ; Search time 4.72103 Seconds (without alignments).
155.808 Million cell updates/sec
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Sequence 25,
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Sequence 15
Sequence 2,
Sequence 3,
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GenCore version 5.1.4\_p5\_4579 Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptcdata/2/laa/5A_COMB.pep:*
/cgn2_6/ptcdata/2/laa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/laa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/laa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/laa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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1 MRVSQIHCALALLGLALAICSQGAA 25
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                                                                                                                                    protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Gaps

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APPLICANT: Keolsch, Gerald
APPLICANT: Lin, Xinli
APPLICANT: Tang, Jordan
TITLE OF INVENTION: Cloning and Characterization of Napsin
NUMBER OF SEQUENCES: 14

INFORMATION:

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NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31,284
       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                     linear
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INVENTION: Cloning and Characterization of Napsin
F SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46; DB 4; Length 445;
Pred. No. 22;
3; Mismatches 9; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 W. Peachtree
STREET: St.
                                                                                                                                                                 3-DOS/MS-DOS
Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                 PRICE APPLICATION NUMBER: US 60/031,196
PRICE APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                       MBER: US 60/046,126
09-MAY-1997
                                                                                                                                                                                                        MBER: US/08/974,691
20-NOV-1997
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6225103
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                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION
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Best.Local Similarity 42.9%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                    COMPUTER READABLE FORM:
                                                             STATE: GA
COUNTRY: USA
TD: 30309-3450
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MEDIUM TYPE: F1
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US-08-974-691-6
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F. Keolsch, Gerald
F. Lan, Win11
F. Tang, Jordan
F. Tang, Cloning and Characterization of Napsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 451;
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2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 42.9%; Pred. No. 23;
Matches 9; Conservative 3; Mismatches
                                                                               APPLICATION NUMBER: US 60/031,196
FILING DATE: 20-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,126
мыек: US/08/974,691
20-NOV-1997
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09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/031,196
FILING DATE: 20-NOV-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JABER: US/08/974,691
20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 OIHMERVKVGSRLTLCAQGCA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 QIHCALALLGLALAICSQGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPAT
OPERATING SYSTEM: PC-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                           404-873-875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                               SEO ID
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Gaps

us-09-727-739b-19.rai

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DB 4; Length 350;
                    Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abbott Laboratories
.00 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRVSQIHCALALLGLALAI 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.1
Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: peptide US-08-637-670-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE MEDIUM TYPE: DI
                                                                                                 LASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barbara G. Ernst
555 13TH STREET, NW Suite 701E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  undman, Olga
VTION: HUMAN ASPARTIC PROTEASES
E: PF-0458-1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: 1906810, GenBank
US-09-705-448-10
                                                                                                                                                                                                                                                                                                                                                      Application US/09705448
                                                                                                                                                                                                                                                254 QVHMESVKVGTGLSLCAQGCS 274
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                                                                                                                                                                                                              5 QIHCALALLGLALAICSQGAA 25
                                                                                                                                               Best Local Similarity 33.3%;
Matches 7; Conservative
419 amino acids amino acids
                                                       ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-974-691-3
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                                                     linear
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APPLICANT: Yu, Guo-Liang
PEPLICANT: Rosen, Craig
TITLE O INVENTE: Colon Specific Genes and Proteins
WUMBER OF SEQUENCES: 24
                                                      Colon Specific Genes and Proteins
                                                                                                                                                 Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
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& Olstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
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Pred. No. 13;
3; Mismatches
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06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application PC/TUS9507289
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IBM PC compatible
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E: Stewart & Olst
6 Becker Farm Roa
                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compat
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Yu, Guo-Liang
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Best Local Similarity 52.9
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Florer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                    ADDRESSEE:
ADDRESSEE:
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APPLICANT: Yu, Guo-Liang
APPLICANT: Rosen, Craig
TITLE OF INVENTION: Colon Specific Genes and Proteins
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carella, Byrne, Bain, Gilfillan, Cecchi,
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N: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, Application US/08469667
5733748
                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-2
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Best Local Similarity 52.9
Matches 9; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                       9 ALALLGLALAICSOGA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                               31 ALACLGLLLAVVSLGS 46
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                                                                                                                           single
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                                    SEQUENCE CHARACTERISTIC
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UTER READABLE FORM:
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INFORMATION FOR SE
SEQUENCE CHARACT
                                                                                                 TYPE: amino a STRANDEDNESS:
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Length 81;

us-09-727-739b-19.rai

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Length 395;
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Coleman, Roger
NVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
                                                      Ouery Match
34.4%; Score 42; DB 1;
Best Local Similarity 38.1%; Pred. No. 80;
Matches 8; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 34.4%; Score 42; DB 2; Best Local Similarity 38.1%; Pred. No. 80; Matches 8; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/723,938
                                                                                                                                                                                                                                                 Sequence 3, Application US/09080538 Patent No. 5965129
                                                                                                                                                              259 OIHMERVKVGPGLTLCAKGCA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J
REGISTATION NUMBER: 36,749
REFERRNCE/DOCKET NUMBER: PF
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 QIHMERVKVGPGLTLCAKGCA 279
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                                                                                                                                                                                                                                                                                                                                                                                                          3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Diskette
IBM Compatible
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SEQUENCE CHARACTERISTICS:
LEBUTH: 395 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                      APPLICANT: Coleman,
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM COOPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                            Palo Alto
                                                                                                                                                                                                                                                                                      INFORMATION:
      ; CLONE: 312099
US-08-723-938-3
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                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 317
CITY: Palo
STATE: CA
COUNTRY: U.
ZIP: 94304
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                                                                                                                                                                                                                 RESULT 12
US-09-080-538-3
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                                                                                                                                                                                                                                                                  DB 5; Length 81;
                                                                                                                                                                                                                                                                                                5; Indels
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APPLICANT: Coleman, Noger
TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS
NUMBER OF SEQUENCES:
ADDRESSEE: Incvtc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASLSEQ VERSION 1.5
RRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,938
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08723938
Patent No. 5776759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TREET: 3174 Porter Drive
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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LENGTH: 395 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                             9 ALALLGLALAICSOGAA 25
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                     5 ALCMLGLVLALLSSSSA 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
                                                                                                   TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415-845-4166
                                                                                                                                                                                                       MOLECULE TYPE: protein PCT-US95-07289-14
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IOR APPLICATION DATA:
APPLICATION NUMBER:
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TYPE: r
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US-08-723-938-3
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tIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                         APPLICATION DATA:
LICATION NUMBER: US 60/031,196
ING DATE: 20-NOV-1996
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Best Local Similarity 38.1%;
Matches 8; Conservative
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                                                                                                                                                                                    0-NOV-1997
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                                                                        COMPUTER READABLE FORM
                                                                                                                                                                            NUMBER:
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                Atlanta
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STREET:
CITY: A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Patrea L. Pabst
2800 One Atlantic Center, 1201 W. Peachtree
                                                                                                                                                                                             HUMAN PROTEASE MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 4;
Pred. No. 85;
4; Mismatches
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5-Jan-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: LUNGASTO1
; SEQUENCE 877617
; SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-09-008-271A-4
                               Application US/09008271A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08974691 Patent No. 6225103
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                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
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                                                                                                                                                                                           TITLE OF INVENTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR
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RESULT 13
US-09-008-271A-4
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) OTHER INFORMATION: 372637, LUNGNOT02 US-09-705-448-1 Ouery Match 34.4%; Score 42; DB 4; Length 420; Best Local Similarity 38.1%; Pred. No. 85; Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps

Search completed: March 21, 2003, 11:42:36 Job time : 5.72103 secs

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Novel G-protein co
Novel G-protein co
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Human protein sequ
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Human aspartic pro-
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Haematopoletic ste
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1.86.
/note= "PPSS-II'' pre-sequence"
26.111
/note= "Mature PPSS-II''"
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Peptide
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Human haematologic
Human ORFX ORF1828
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Rainbow trout pr
Rainbow trout pr
Enolase protein
                                                                                                                 March 21, 2003, 14:35:23 ; Search time 15.4506 Seconds (without alignments) 215.607 Million cell updates/sec
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being printed,
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/SIDSI/gcgdata/yeneseqy/geneseqp-embl/AA2000.DAT
/SIDSI/gcgdata/yeneseqy-embl/AA2001.DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT
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                                                                                                                                                                                                                                                                                                                                                                                               908470
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                          hits satisfying chosen parameters:
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1 MRVSQIHCALALLGLALAICSQGAA 25
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-Maximum Match 100%
Listing first 45 summaries
                                                                                  protein search, using sw model
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AAM81978
AAB42064.
AAW54357
ABB57379
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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"ppss-II'' pro-sequence" 7.00c= From It of Sequence 87.111 Frosomatostatin II'' 96.97

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an Oncorhynchus mykiss somatostatin polypeptide containing a portion of preprosomatostatin (PPSS-11) and/or a portion of preprosomatostatin (PPSS-11) and/or a portion of preprosomatostatin and their associated polynuclectides are useful for identifying modified sometostatin polypeptide which functions as somatostatin agonist useful for research, therapeutics or diagnostics, including medical and verteinary applications: The wild-type somatostatin and its modified verteinary applications in wild-type somatostatin and its modified verteinary applications. The wild-type somatostatin and its modified the pituitary (e.g. acromagaly) or gastroenteropancreatic tissues (e.g. gastrinoma, glucagonoma, carcinoloid syndrome), to cause tumour shrinkage through their effects on cell proliferation and apoptosis and as adjuncts and glucagon. In addition, dysfunctional somatostatin secretion; and glucagon in addition, dysfunctional somatostatin secretion. Is associated with acquired immunodeficiency syndrome (ADS) and various neurological disorders (e.g. epilepsy, Alzhelmer's disease and their metastases) and somatostatin attagonists are effective in the treatment of such conditions. Nucleic acids encoding the polypeptides are useful in gene therapy and fusion peptides can be targeted to neoplasms and their metastases, inhibiting the release of their sequence represents O. Wakiss pressor of their secretory products. Note the sequence represents O. Wakiss pressor of their secretory products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New somatostatin polypeptides derived from Oncorhynchus myklss, to for treating diabetes mellitus, acromegaly, gastrinoma, acquired immunodeficiency syndrome and neurological disorders -
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"Dibasic cleavage site"
                             98.111
/note= "SS-14 variant peptide"
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Local Similarity 100.0%; ins 25; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                          RES FOUND
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N-PSDB; AAS12935.
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specification.
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                                                                                                                                                                                                                                                                                                                                           03-DEC-1999;
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Matches 25
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The invention relates to an Oncorhynchus mykiss somatostatin polypeptide containing a portion of preprosomatostatin [PESS-ID] and/or a portion of preprosomatostatin and of preprosomatostatin and portion of preprosomatostatin and polypeptide which functions as a somatostatin agonist useful comparability of preprosoration applications. The wild type somatostatin and applications. The wild type somatostatin and its modified for research, therapeutics or diagnostics, including medical and control of the pitultary (e.g. acromegaly) or gastroenteropancreatic tissues (e.g. gastrinoma; alucagon as cardinoid syndrome,), to cause tumour shrinkage of plucagon. In addition, dysfunctional somatostatin secretion is and glucagon. In addition, dysfunctional somatostatin secretion is neurological disorders (e.g. epilepsy, Alzheimer's disease and Huntington's disease) and somatostatin antagonists are effective in the treatment of such conditions. Nucleic acids encoding the polypeptides are treatment of such conditions. Nucleic acids encoding the polypeptides are custul, in gene therapy and fusion peptides can be targeted to neoplasms or understases, inhibiting the release of their secretory products. This sequence represents O Mykiss PPSS-II (protein.
neurological disorder; HIV;
        glucagon; acquired immunodeficiency syndrome; neurological disorder; HIV epilepsy, Alzheimer's disease; Huntington's disease; neuroprotective; neoplasm; metastasis; gene theriapy; antidiabetic; nootropic; cytostatic; anti-human immunodeficiency Virus; osteopathic; anticonvulsant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New somatostatin polypeptides derived from Oncorhynchus myklss, u
for treating diabetes mellitus, acromegaly, gastrinoma, acquired
immunodeficiency syndrome and neurological disorders
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/note="Dibasic cleavage site"
102...115
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101
ote- "PPSS-II' pro-sequence"
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1.25
/note= "Signal peptide"
1.87
/note= "PPSS-II' pre-sequ
                                                                                                                                                                                                                                                                                                                                                                                          ressell' pre-sequence .26_115
/hote= "Mature PPSS-II'"
Misc-difference 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NDSU-) NDSU RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
88.115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-425997/46.
N-PSDB; AAS12934.
                                                                                                                                                                                           Oncorhynchus mykiss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sheridan MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-2001:
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PPSS-II'; PPSS-II'; endocrine tumour; pituitary gland; glucagonoma; AIDS; glastoceneropencreatic tissue; accomegaly; gastriona; dlabetes mellitus; carcinold syndrome; cell proliferation; apoptosis; growth hormone; glucagon; acquired immunodeficiency syndrome; neurological disorder; HIV; epilepsy; Alzheimer s disease; funtington's disease; neuroprotective; neoplasm; metastasis; gene therapy; antidiabetic; nootropic; cytostatic; anti-human immunodeficiency virus; osteopathic; anticonvulsant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an Oncorhynchus mykiss somatostatin polypeptide containing a portion of preprosomatostatin I (PPS-I) and/or a portion of preprosomatostatin II (PPS-II) whe protein sequences and their associated polynucleotides are useful for identifying modified somatostatin polypeptide which functions as a somatostatin aponist useful for research, therapeutics or diagnostics, including medical and veterinary applications. The wild-type somatostatin and its modified
                                                                                                                                                                                                                                                                                                                                                                                                             Rainbow trout; somatostatin; preprosomatostatin; hypersecretion; PPSS-I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iry applications. The wild-type somatostatin and its modified
are useful for treating hypersecretion from endocrine tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New somatostatin polypeptides derived from Oncorhynchus mykiss, u
for treating diabetes mellitus, acromegaly, gastrinoma, acquired
Immunodeficiency syndrome and neurological disorders
     ö
     Indels
                                                                                                                                                                                                                                                                                                                                                           Rainbow trout preprosomatostatin I (PPSS-1) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.100
'note- "Dibasic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .100
rie- "PPSS-I pro-sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..88
note= "PPSS-I pre-sequence"
  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114
te- "Prosomatostatin I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...24
'note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.114
note= "Mature PPSS-I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kittelson JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "SS-14 peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                 AAU07666 standard; Protein; 114 AA.
                                               1 MRVSQIHCALALLGLALAICSQGAA 25
                                                                     Claim 1; Fig 2; 52pp; English
                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "F7
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moore CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncorhynchus mykiss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-425997/46.
N-PSDB; AAS12933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA2325169-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sheridan MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NDSU-) NDSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-DEC-1999;
                                                                                                                                                                                                                                                                                                              04-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUN-2001.
22;
                                                                                                                                                                                                                                                              AAU07666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       version
                                                                                                                                                               AAU07666
ID
Matches
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the antigenicity

Sequence

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in the treatment of diabetes mellitus via inhibition of growth hormone and glucagon. In addition, dysfunctional somatostatin secretion is associated with acquired immunodeficiency syndrome (ALDS) and various neurological disorders (e.g. epilepsy, Alzheimer's disease and Huntington's disease) and somatostatin antagonists are effective in the treatment of such conditions. Nucleic acids encoding the polypeptides are useful in gene therapy and fusion peptides can be targeted to neoplasms and their metastases, inhibiting the release of their secretory products. This sequence represents 0. Mykiss PPSS-I protein.

Note: The features for this sequence are specifically claimed in the specification.
                                                                                                                                                                                                                                                                                                                                                                          ö
the pituitary (e.g. acromegaly) or gastroenteropancreatic tissues (e.g. gastrinoms, glucagonoma, carcinold syndrome), to cause tumour shrinkage through their effects on cell proliferation and apoptosis and as adjuncts in the treatment of diabetes mellitus via inhibition of growth hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the wild type human enolase (NSE) protein. The primers represented by AAT60282-7660285 were used to amplify tyrosine introduced versions of this sequence. The introduced tyrosine residues combine a radioisotope in such a way as to have no substantial effect on the antigencity of the protein. The peptides with the introduced tyrosine residue are prepared by expressing a recombinant DNA sequence, where the tyrosine residue has been introduced via an insertion or substitution into the wild type sequence. The peptides can then be used in radioimmunoassays, as the introduction of the label does not alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR; polymerase chain reaction; primer; amplify; tyrosine; human; NSE; enolase; radioisotope; antigen.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Introducing tyrosine residues into a protein for radioisotopic labelling – by substitution, addition and/or insertion to a DNA coding for the protein, antigenicity of the protein is unchanged by
                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                             Score 64; DB 22; Length 114;
Pred. No. 0.048;
3; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 10-11; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW14001 standard; Protein; 433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRVSQIHCALALLGLALAICSQGAA 25
                                                                                                                                                                                                                                                                                                                             52.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95JP-0145542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 60.0
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EIKE ) EIKEN KAGAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-059703/06.
                                                                                                                                                                                                                                                                                         114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enolase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP08308584-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW14001;
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                               Qúery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW14001
ID AAW1
XX
AC AAW:
XX
DT 23-P
XX
DE EDO.
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us-09-727-739b-19.rag

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The present invention relates to compositions and methods for the detection, diagnosis and therapy of haemaclogical malignancies. The present sequence is the protein sequence of a human haematological malignancy related antiden. The methods of the present invention comprise melognancy related antiden. The methods of the present invention comprise detecting the presence of hematological malignancy related antique(s) in polypeptide, compared to an unaffected individual, is indicative of an increased risk; Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukacmia, lymphoma, tolicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
                                                                                                                                                                                                                                                                                     haematological malignancy; antigen; chronic lymphocytic leukaem
follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma
                                                                                                                                                                                                                                                             vascular; gene therapy; vaccine; lymphoma; ignancy; antigen; chronic lymphocytic leuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, flymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 120;
                                                                                                                                                                                                          Human haematological malignancy-related antigen #1611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ore 48; DB 22;
ed. No. 12;
Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48;
Pred. No. 1
                                                        AAM81913 standard; Protein; 120 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1152; 1252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM81978 standard; Protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaiger A, Algate PA, Mannion J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.3%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001; 2001WO-US07272
                                                                                                                                                          13-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 ANAILGVSLAVCKAGA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 ALALLGLALAICSOGA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-514842/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
Les 9; Conserv
                                                                                                                                                                                                                                                             Human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                               WO200164886-A2.
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                           AAM81913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM81978
ID AAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein, cDNA and genomic sequences of a human enolase 3 (beta, muscle) isogene containing a number of single nucleotide polymorphisms (SNPs). The sequences can be used to identify the haplotype of an individual and identify whether particular haplotypes are linked to certain diseases. The present sequence is the ENO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; enolase 3(beta, muscle); ENO3; single nucleotide polymorphism; SNP; haplotype analysis; isogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel genetic variants of enolase 3, (beta, muscle) gene useful in studying expression and function of the protein, and for screening drugs to treat disorders of glycolytic pathway
     DB 18; Length 433; 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23; Length 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52; DB
Pred. No. 12;
4; Mismatches
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note- "optionally Val"
        Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "optionally Ser"
Misc-difference 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "optionally Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "optionally Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duda A, Finkel K, Koshy B, Parks KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human enolase 3(beta, muscle) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key. Location/Qualifiers
Misc-difference 71
                                                                                                                                                                                                                                                                                     AAM48922 standard; Protein; 434 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; Fig 3; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENA-) GENAISSANCE PHARM INC.
     42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-US20952.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2000; 2000US-215236P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-154721/20.
N-PSDB; AAK98531, AAK98532.
                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 ANAILGVSLAVCKAGAA 124
                                                                                                                                      107 ANAILGVSLAVCKAGAA 123
                                                                                                     9 ALALLGLALAICSQGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALALLGLALAICSOGAA 25
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 332
Query Match
Best Local Similarity
Matches: 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434 AA;
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WO200202579-A2.

10-JAN-2002.

16-APR-2002

AAM48922;

RESULT 5

ð Dp follicular

Gaps

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the haplotype care linked to protein.

X X C C C C C X X Q

Sequence

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a ò

08-FEB-2001 (first entry)

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The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen. The methods of the present of the presence of haematological malignancy related antigen(s) in polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma.
                                                                                                                                            Human; cytostatic; vascular; gene therapy; vaccine; lymphoma; haematological malignancy; antigen; chronic lymphocytic leukaem follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.3%; Score 48; DB 22; Length 162; 56.2%; Pred. No. 17; 3; Indels 1.1ve 4; Mismatches 3; Indels
                                                                        Human haematological malignancy-related antigen #1676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 1178; 1252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mannion J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001; 2001WO-US07272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0186126
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-514842/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 AA;
                                                                                                                                                                                                                                                                                                                                                                 WO200164886-A2.
                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          07-SEP-2001.
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AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
sequences have activities such as: cytostatic; hepatotropic; vulnerary;
antipacriatic; anticonvulsant; antiarthritic; immunosuppressant;
immunostimulant; cardiant; thrombolytic; coaquiant; vasotropic;
antidiabetic; hypotensive; dermatchlogical; immunosuppressive;
antidiahetic; hypotensive; dermatchlogical; immunosuppressive;
antidificialmantory; antibacterial; antivital; antifinantic;
antidificialmantory; antibacterial; antivital; antifinantic;
antidificialmantory; antibacterial; antivital; antifinantic;
antidificialmantory; antibacterial; antivital;
antidificialmantory; antibacterial; antivital;
antidificialmantory; manufacterial; antivital;
antidificialmantory; antibacterial; antivital;
antidificialmantory; antibacterial; antivital or treating
pathological conditions associated with an ORFX associated disorder. The
nucleic acids can be used to express ORFX proteins in gene therapy
vectors. The proteins and nucleic acids may be used to treat cancers;
correctors. The proteins and nucleic acids may be used to treat cancers;
antidiated disorders, neurodegenerative disorders, osteoarthritis;
and the acidical acidic
                                                                                        Human: open reading frame, ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; noctropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunosuppressant; cardiant; immunosuppressive; dematological; immunosuppressive; antificiametory; antivaral; antibacterial; antificiangal; antirhematic; antitinamatory; antivaral; antibacterial; antificiangal; antirhematic; antithyroid; antificiandantc; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiancy; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; thrombosis; contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 48;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
Human ORFX ORF1828 polypeptide sequence SEQ ID NO:3656.
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56.28; Pred
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02-APR-1999; 99US-0127636
05-APR-1999; 99US-0127728
30-MAR-2000; 2000US-0540763
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N-PSDB; AAC76273.
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Best Local Similarity
Matches 9; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 429 AA;
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AAB42064 standard; Protein; 429 AA

RESULT 8 AAB42064

AAB42064;

SXXX

| |:||::||:| || 109 ANAILGVSLAVCKAGA 124

. qq

24

9 ALALLGLALAICSOGA

Best Local Similarity 56.2 Matches 9; Conservative

AAW54357;

RESULT 9

ò qq

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modified expression in fetal heart tissue as compared to adult heart tissue and the encoded proteins (ABB57375.ABB57392). The genes have cardiant activity and may be useful in the promotion of the repair of damage to heart tissue caused by myocardial necrosis. The gene sequences are useful for screening potential compounds for the ability to influence disease associated with myocardial necrosis. Drugs identified by the screening methods may be used to treat and prevent disease with which myocardial necrosis is associated, such as cardiac hypertrophy and cardiac insufficiency. Diagnosis of diseases such as those above is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                              Genes having differential expression in fetal and adult heart tissue useful for screening potential drugs for promoting repair of damage caused by myocardial necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to gene sequences (ABI99915-ABI99934) having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 48; DB 23; Length 434;
Pred. No. 49;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia pneumoniae protein not found in C. trachomatis
                                                                                                                                                                                                                                                                            Sakurada K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 53; Page 98-100; 171pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY35223 standard; Protein; 210 AA
                                                                                                                                                                                                                                                                            Kikuchi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.3%;
llarity 56.2%;
Conservative 4
                                                                                                                          27-APR-2001; 2001WO-JP03700.
                                                                                                                                                                                                                            (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                           27-APR-2000; 2000JP-0126741.
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97FR-0014673.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                            Sekine S,
                                                                                                                                                                                                                                                                                                                       WPI; 2002-075160/10.
N-PSDB; ABI99919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      434 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
Matches 9; Conserv
                         WO200183705-A1
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21-NOV-1997;
                                                                             08-NOV-2001.
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                                                                                                                                                                                                                                                                         Yamada Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disclosed.
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AAY35223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      these proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat mucocardial cell proliferation associated polypeptide SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ometrium during the hyperplassia, adenocarcinoma or proliferative se of the endometrium. The presence and guantities of these protein be detected using 2D gel electrophoresis comparison of cell lysate proteins can be used as biochemical markers to detect the phase of endometrium and can be measured in body fluids, obviating the need
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins. AAW54349-W54364 are examples of proteins produced in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                        Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
2D gel electrophoresis; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 19; Length 433; 48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemical markers of human endometrium - udiagnosis of hyperplasia and adenocarcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB57379 standard; Protein; 434 AA.
                                                                                                                                                                        AAW54357 standard; protein; 433 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Larsen P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97GB-0007132.
96GB-0018600.
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                                  103 ANAILGVSLAVCKAGA 118
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9 ALALLGLALAICSOGA 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-207057/18.
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                                                                                                                                                                                                                                                                                                                          Alpha Enolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9810291-A1.
                                                                                                                                                                                                                                                                         14-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-1997;
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06-SEP-1996;
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phase of the
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ABB57379;

Sequence

Query Match

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Gaps

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The invention relates to 1 of 232 isolated or recombinant polynuclectides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynuclectide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An isolated or recombinant polynucleotide used to produce a transgenic plant -
  in signal transduction after ligand binding. These NGPCR's are expressed in human placenta, bone marrow, trachea, testis, liver and kidney cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               microbial discusse resistance, herbicule resistance; drought; fruit yield; growth rate; leaf senescence; flower senescence. plant; transcription factor; transgenic.
                                                                                         DB 23; Length 423;
67;
                                                                                                                                                6; Indels
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, Yu G, 1
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                                                                                                         1larity 45.0%; Score 47; DB 45.0%; Pred. No. 67; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 40; Page 864-866; 941pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis transcription factor #210.
                                                                                                                                                                                                                                                                                                      AAU93172 standard; Protein; 472 AA
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PILGRIM M.
CREELMAN R.
DUBELL A J.
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Ratcliff O, Reuber JL,
                                                                                                                                                                                                     142 LSNVGCALSVTGLALTVIFQ 161
                                                                                                                                                                        3 VSQIHCALALLGLALAICSQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-2000; 2000US-227439P.
16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
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                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-292022/33
                                                                         423 AA;
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                                                                           Sequence
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(PILG/)
(CREE/)
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(RIEC/)
(YUGG/)
(PINE/)
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AAU93172
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pneumoniae
                                                                                                                   AAY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AAX91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent ofitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AAY34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors, containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated G-protein coupled receptor polypeptide useful for identifying compounds that modulate the protein expression or activity which are used to treat a variety of physiological or mental disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequences given in AAB47761-69 show novel G-protein coupled receptor (NGPCR) polypeptides. The NGPCR coding sequences are found on chromosome 3 at 3811.1 in the human genome. These NGPCR proteins show the presence of 7 conserved transmembrane domains which are interconnected by non-conserved hydrophilic loops. They are involved
                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel G-protein coupled receptor; NGPCR; transmembrane domain; signal transduction; ligand bindhing; human; placenta; bone marrow; trachea; testis; liver; kidney cell.
                                                                                                                                                                                                                                                                                                                                                                   Similarity 45.08; Pred. No. 32; 9; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                     Page 1070-1071; Disclosure; 1912pp; English.
                                                  Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 78-79; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 EIASAIAILGLLVAFCASAA 67
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                WPI; 1999-357842/30.
                                                                                                                                                                                                                                                                                                                                     210 AA;
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                                                                                                                                                                                                                                                                                                                                       Sequence
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Best Local
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AAB47765
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27-APR-2001; 2001WO-US13371.
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             Pilgrim M,
Adam L, Ra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                               plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the polypeptide or antisense nucleic acid, thereby producing a modified plant, and selecting for a modified trail (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolorance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 proteins which are a thallane transcription factors:
                   associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information, and identifying an esquence specification in the specification. The isolated of fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide or antisense nucleic acid, inserting the polynucleotide or antisense nucleic acid, into a expression vector, introducing the vector into a plant to a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified
ectopic expression or altered expression of one or more genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microbial disease resistance; herbicide resistance; seed yie
fruit yield; growth rate; leaf senescence; flower senescence
plant; transcription factor; transgente.
                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 23; Length 472;
Pred. No. 75; 6; Indels
7; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agriculture; metabolic chemical; environmental microbial disease resistance; herbicide resista
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis transcription factor #56
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16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
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                                                                                                                                                                                                                                                                                                                                                                                           Juery Match 38.55
Jest Local Similarity 40.9
Matches 9: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
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The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, tippir variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered to a wholytype as compared to a wild-type or reference plant, or the plant exhibits and altered exhibits ectopic expression or altered expression of one or more genes associated with a plant tait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of recombinant polynucleotide is used for producing a plant having a recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide, or an antisense nucleic acid, inserting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 proteins which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oolynucleotide or antisense nucleic acid into an expression vector, introducing the vector into a plant or a cell of a plant to overexpress
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    Keddie J;
Pineda O;
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    , Heard J, Jiang C,
Riechmann JL, Yu G,
                                                                                                                                                                                                                                An isolated or recombinant polynucleotide used
                                                                                                                                                                                                                                                                                                                                              Claim 40; Page 265-267; 941pp; English.
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Dubell AJ,
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                                            Reuber JL,
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illarity 40.9%;
Conservative
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        Creelman R,
                                       Ratcliff O,
                                                                                                              WPI; 2002-292022/33
N-PSDB; ABK65204.
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Best Local Similarity
Matches 9, Conserv
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Walke DW, Scoville J; Wang X,

(LEXI-) LEXICON GENETICS INC.

WPI; 2002-049266/06. N-PSDB; AAI72009.

Novel isolated G-protein coupled receptor polypeptide useful for identifying compounds that modulate the protein expression or activity which are used to treat a variety of physiological or mental disorders

Claim 6; Page 77; 85pp; English.

The sequences given in AAB47761-69 show novel G-protein coupled receptor (NGPCR), polypeptides. The NGPCR coding sequences are found on chromosome 3 at 3411.1 in the human genome. These NGPCR proteins show the presence of 7 conserved transmembrane domains which are interconnected by non-conserved hydrophilic loops. They are involved in signal transduction after ligand binding. These NGPCR's are expressed in human placenta, bone marrow, trachea, testis, liver and kidney cells.

481 AA; Sequence

Gaps Query Match 38.5%; Score 47; DB 23; Length 481; Best Local Similarity 45.0%; Pred. No. 76; Matches 9; Conservative 5; Mismatches 6; Indels 6; Indels

3 VSQIHCALALLGLALAICSQ 22 :| :| || :| || :| | 200 LSNVGCALSVTGLALTVIFQ 219 qq ò

Search completed: March 21, 2003, 11:38:04 Job time: 17.4506 secs